

STIC Database Tracking Number 115405

TO: James Schultz

Location: REM/2D 182C18

Art Unit: 1635

Monday, March 01, 2004

Case Serial Number: 09/904568

From: Toby Port

Location: Biotech-Chem Library

Remsen 1A59

Phone: 571-272-2523

toby.port@uspto.gov

Search Notes

Dear Examiner Schultz,

Here are the results of your search.

Please feel free to contact me if you have any questions.

Toby Port





STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor 571-272-2507 Remsen E01 D86

VO	untary Results Feedback English
>	I am an examiner in Workgroup: Example: 1610
۶	Relevant prior art found, search results used as follows:
	☐ 102 rejection
	☐ 103 rejection
	☐ Cited as being of interest.
	Helped examiner better understand the invention.
	Helped examiner better understand the state of the art in their technology.
	Types of relevant prior art found:
	Foreign Patent(s)
	Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.)
>	Relevant prior art not found:
	Results verified the lack of relevant prior art (helped determine patentability).
	Results were not useful in determining patentability or understanding the invention.
Co	mments:

Drop off or send completed forms to STIC/Biotech-Chem Library Remsen Bldg



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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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ABZ48702
ABZ43362
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AAL33664
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                                                                                                                                                                             Aat89912
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                               Aaa49970
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                                                                      Human gra
Human SNP
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Primer 17
Human N-m
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Streptavi
C allele
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Permutein
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Leu
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ALIGNMENTS

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RESULT 1
AAT89912/c
ID AAT89912;
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AC AAT89912;
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AC AAT89912;
XX

CAPR-1998 (first entry)
DT 14-APR-1998 (first entry)
DT 14-APR-1998 (first entry)
XX

DE Human ubiquitin carrier protein,
XW
Ubiquitination; cell cycle
XW
Ubiquitination; cell cycle
XW
Ubiquitination; cell cycle
XW
Ubiquitination;
XX

OS Synthetic
OS Synthetic
OS Homo sapiens
XX

XX

09-OCT-1997;
YM

DO-OCT-1997;
YM

PD 09-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human ubiquitin carrier polypeptide UbcH10 primer HSEAUC:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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97US-00820639.
97US-00828533.
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U1 epitope;
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PCR antisense primer HSEAUC (AAT89912) encodes the last 6 amino acids of the open reading frame (see AAT89895) of UbcH10 (see AAW11277), a novel human ubiquitin carrier protein that is involved in the ubiquitination and degradation of mitotic cyclins. HSEAUC also encodes the amino acids DTYRYI (AUI epitope) and includes 2 stop codons and an HindIII restriction site. It was used with sense primer HSEN (see AAT89910) to

e E

New ubiquitin carrier polypeptide(s) cyclin A and cyclin B and are useful proliferation.

- are involved in ubiquitination of to screen for new inhibitory of cell

Α,

Kirschner MW,

Townsley

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Example 8; Page 86; 138pp; English

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Query Match
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Matches 26
          The preparation of biologically-activated circularly-permuted proteins ((permuteins) comprises the use of a method comprising making a series of circularly permuted genes. The circularly permuted genes are inserted conton a display vector, where they are expressed so that the proteins they cancode are presented on the surface of the display vector. A library of contone are presented in the surface of the display vector. A library of contone are presented in the surface of the display vector. A library of contone are presented in the surface of the display vector. A library of contone are protein that can bind a biologically active contone in the surface of the display vector. The presenting contone is solded and contone to the structure of a parent protein. The permuted protein to the structure of a parent protein, a segment derived from the carboxy portion of the parent protein, a segment consisting of a comparent form the amino terminus of the parent protein, and a linker or constitute sequences AAA3556-A35943 encode linkers used to create the permuteins of the invention. The method is used to generate libraries of permuteins with improved therapeutic properties compared to their parent parent constituted as antispens for producing antibodies which are used in immunology or immunotherapy as probes or intermediates used to construct other useful permuteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 48
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                                                                                                                                                                                                                                                                                                                                                                                                        Preparation of biologically-activated circularly-permuted proteins by scanning permutagenesis for generating libraries of permuteins with improved therapeutic properties.
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83.9%;
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     therapeutic
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RESULT 4
AAZ44243
ID AAZ4
XX

AAZ44243

standard; DNA;

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                                                                                                                                                                                                                          The present invention describes a nucleic acid which encodes an anti-My-
10 antibody. The present sequence represents a PCR primer for the H chai
variable region of the antibody. Also described is a method for the
production of a recombinant antibody in which the above nucleic acid is
used to produce an antibody which combines with human CD34 antigen by
gene recombinant on. The anti-CD34 antibody gene is used to produce
recombinant anti-CD34 antibodies efficiently, which can be used in
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antibody; heavy; li
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    CCCAGCCGGCCATGGCCCAGGTGCAGCTGAAGCAGTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  dy against human CD34 - and nucleic acid production of the antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chain variable region;
ht; CDR; human CD34 ant:
                                                                                                     3.2%;
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                                                                                                                                                                       16 G; 4 T; 0 U; 0 Other;
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mouse anti-My-10 PCR primer
                                                                                  Score 21.4; DB 2;
pred. No. 1.2e+05;
0; Mismatches 11
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No. 6
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antigen; hyk
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RESULT 5
AAL28467
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Best Local :
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                                  Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; neuroprotective; antiinflorobial; gene therapy; vaccine; amylase; cancer; amyloid protein; angiopoietin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinase; cytokine; interferon; interfeukin; G-protein coupled receptor; thioesterase; inflammation; interfeukin; G-protein coupled receptor; thioesterase; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel device (I) for separating cluster differentiation (CD)-positive cells using a recombinant (chimeric or single-chain) antibody recognising CD4 or CD34. The devices are useful for the separation of CD4 or CD34 positive cells, which is useful for the collection of hematopoietic undifferentiated cells, elimination of collection of hematopoietic undifferentiated cells, elimination of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia; hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation; HIV infection; autoimmune disease; murine; primer; ss.
          multifactorial disease; autoimmune nervous system disease; ss.
                                                                                                                                       Human SNP oligonucleotide #1675.
                                                                                                                                                                    24-JAN-2002
                                                                                                                                                                                               AAL28467
                                                                                                                                                                                                                          AAL28467 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example
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(ASAH )
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26-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       detection
                                                                                                                                                                                                                                                                                                                                                                                                                                         ymphocytes from cells to be used in bone marrow transplantation, the stection of leukemic cells and the production of medicinal compositions or the treatment of HIV infection and autoimmune diseases. AA24237-44246 represent primers used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                          513
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ASAHI
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                                                                                                                                                                                                                                                                                                                            CCCTGCAGCCGAGCGTCCTGATGCAGCTGAAGCTTTCAG
                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               BP; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 54; 111pp; Japanese.
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98JP-00163023.
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                                                                                                                                                                  entry)
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Pred. No. 1.2e
0; Mismatches
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                         disease;
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                                                                                                                                                                                                                                                                                                                                                                                 DB 3;
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AAX19291/c
ID AAX19291
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AC AAX19291;
AC AAX19291;
DT 17-MAY-19
XX
Human gra
XX
Human; gr
KW Human; gr
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Synthetic
OS Synthetic
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Homo sapi
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WO9853072
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PN WO9853072
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PD 26-NOV-19
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PF 21-MAY-19
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Best Local S
Matches 31
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protein coupled receptors and thioesterases. The present sequence is one
such oligonuclectide. The oligonuclectides and the peptides encoded by
them may be used in the prevention, diagnosis and treatment of diseases
associated with inappropriate expression of the proteins listed above.
Disorders that may be prevented, diagnosed and/or treated include
multifactorial diseases with a genetic component, such as autoimmune
diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
systemic lupus erythromatosus and Grave's disease), inflammation, cancer
(e.g. cancers of the bladder, brain, breast, colon and kidney,
leukaemia), diseases of the nervous system and an infection of pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polymorphic nucleic acids encoding e.g. amylases, oncogenes and histones, useful for diagnosing and autoimmune diseases and infections.
               21-MAY-1998;
                                           26-NOV-1998
                                                                         WO9853072-A1
                                                                                                  Synthetic.
Homo sapiens
                                                                                                                                              Human; granulocyte colony-stimulating haematopoiesis disorder; primer; ss.
                                                                                                                                                                                                                       17-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoiet apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1;
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27-DEC-2000; 2000US-00173419.
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                                                                                                                                                                                        granulocyte colony-stimulating
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                                                                                                                                                                                                                                                                                standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 1859; 4143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                  AGTGGCCGAGTGAGTTTCTTGGGGGCCCCAGCTTCCTCCAGAGGTGGC
                                                                                                                                                                                                                                                                                                                                                        AGGGGCAGACTGGGCAGTGGGGAGCCCCATCGTGCCCCAGAGGTGGC
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                 98WO-KR000125
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0; Mismatches
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Pred. No. 1.
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                                                                                                                                                                                          factor antisense primer oligo
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                                                                                                                                                            factor; G-CSF;
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                                                                                                                                                                                                                                                                                                                                                                                                                 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pathogenic
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RESULT 7
AAL33664/c
Query Match
Best Local S
Matches 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    granulocyte colony-stimulating factor (hg-CSF). The present invention also describes: (1) recombinant plasmid pYMM-G-CSF containing the cDNA for the peptide; and (2) E. coli BL21 (pYMM-G-CSF) (KCTC 0477BP) transformed with the plasmid. The plasmid and E. coli strain are used to produce high yields of highly purified hg-CSF, which when refolded has comparable biological activity of G-CSF, hg-CSF is used to treat haematopoiesis disorders. The method of producing hg-CSF is less time-consuming and, therefore, more economical than previous methods because the protein is expressed in high yields without the need for further processing steps. AAX19290 to AAX19315 represent primer used in the synthesis of hg-CSF from an example of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human granulocyte colony-stimulating factor (hg-CSF) containing a peptide at the N-terminus - useful in the treatment of haematopoiesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human SNP oligonucleotide #6872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAL33664 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes the N-terminal peptide of human granulocyte colony-stimulating factor (hG-CSF). The present inv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Fig 1; 19pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-131691/11.
                                                                                             28-DEC-1999; 99US-0173419P
27-DEC-2000; 2000US-00173419
                                                                                                                                                      28-DEC-2000; 2000WO-US035498
                                                                                                                                                                                                                                   WO200147944-A2
                                                                                                                                                                                                                                                                         Homo sapiens
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(JEIL-) JEIL I
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                                                        (CURA-) CURAGEN CORP.
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29; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCCACGGGTCCTGCCAGCTCCCTGCCGCAGAGCTTCCTGCT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВP
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No. 1.
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د
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В Ś

3.0

Shimkets RA,

Leach M;

Polymorphic nucleic acids

encoding e.g.

amylases,

cyclins,

polymerases.

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PACACA A SACA A 
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Best Local
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protein coupled receptors and thioesterases. The present sequence is one
such oligonucleotide. The oligonucleotides and the peptides encoded by
them may be used in the prevention, diagnosis and treatment of diseases
associated with inappropriate expression of the proteins listed above.
Disorders that may be prevented, diagnosed and/or treated include
multifactorial diseases with a genetic component, such as autoimmune
diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
systemic lupus erythromatosus and Grave's disease), inflammation, cancer
(e.g. cancers of the bladder, brain, breast, colon and kidney,
leukaemia), diseases of the nervous system and an infection of pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer, amyloid protein; anglopoletin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating facto complement related protein; cytochrome; kinesin; cytokine; interferon; interleukin; G-protein coupled receptor; thioesterase; inflammation; multifactorial disease; autoimmune disease; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer autoimmune diseases and infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           multifactorial disease; nervous system disease;
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27-DEC-2000;
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                                                       WPI; 2001-465210/50
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2000US-00173419.
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Pred. No. 1.4e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer;
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Claim 1; Page 3315; 4143pp; English

diseases

and

intections.

oncogenes and histones, useful for diagnosing and treating, e.g. cancer

Page 180;

2785pp;

English

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RESULT 9
ABZ49057/c
ID ABZ490
XX ABZ490
XX ABZ490
XX POLYMO
XX POLYMO
XX Human;
XW POLYMO
XW Geneti
XW Gilnic
XX Homo s
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Best Local
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Identifying individuals having a polymorphism, useful for determining the effectiveness or side effect of a drug or treatment protocol, comprises detecting at least one polymorphism in the drug metabolizing enzyme
                                                                                                                                                                           Nakamura
                                                                                                                                                                                                                                                                                            27-DEC-2000; 2000JP-00399443
02-MAY-2001; 2001JP-00135256
27-AUG-2001; 2001JP-00256862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200252044-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; drug metabolising enzyme; gene; drug metabolism; chromosome polymorphic site; drug evaluation; drug screening; genotyping; genetic profiling; therapeutic customisation; adverse reaction; clinical trial; drug approval; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                   27-DEC-2001; 2001WO-JP011592.
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Sequence 40

BP; 6 A; 15 C; 9

G; 10 T; 0 U; 0 Other;

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CC drugs. SNPs are also useful as polymorphism markers for discovering genes and that cause or exacerbate certain diseases. SNPs are particularly useful in the above respects as they are stable in populations, occur frequently, and have lower mutation rates than other genome variations are particularly useful in the above respects as they are stable in populations, occur frequently, and have lower mutation rates than other genome variations are such as repeating sequences. The detection and analysis of polymorphisms are such as repeating drug metabolising enzymes allows the customisation of any therapies based upon the genetic profile of individual patients.

CC This would not only take the guesswork out of selecting the drug with the greatest therapeutic effect for a particular patient, but would also reduce the likelihood of adverse reactions, thereby increasing safety. CC methods of the invention are also useful in the drug discovery and comproval processes. For example, individuals could be selected for approval processes. For example, individuals could be selected for appropriate patient populations. The methods, data and compositions of the invention may therefore lead to an increase in the range of composition patient populations. The methods, data and compositions of the invention and the number of different medications, failed drug trials, the time taken for a drug to be approved, the length of time patients are on medication and the number of different medications a patient needs to take before finding an effective therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               variety of detection assays, including hybridisation assays, nucleic acid arrays and PCR-based methods. The invention also encompasses methods of evaluating and screening drugs using genetic polymorphism data. Genetic polymorphism data, particularly that relating to single nucleotide polymorphisms (SNPs), may be used in studying the relationship between DNA sequence variations and human diseases, conditions, and responses to drugs. SNPs are also useful as polymorphism markers for discovering genes that cause are also useful as polymorphism markers for discovering genes that cause are also useful as polymorphism markers for discovering genes that cause are also useful as polymorphism markers for discovering genes that cause are also useful as polymorphism confidence.
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RESULT 10
ABZ46527/c
ID ABZ465
XX ABZ465
XX ABZ465
XX 26-JUN
XX 26-JUN
XX Human.
XX Human.
XX Encic
XX Genetic
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Best Local
                                                                                                                                                                               Human; drug
polymorphic
genetic prof
                                                                                                                                                             Hyman; drug metabolising enzyme; gene; drug metabolism; chromosome polymorphic site; drug evaluation; drug screening; genotyping; genetic profiling; therapeutic customisation; adverse reaction; clinical trial; drug approval; ds.
                                                                                                                                                                                                                                                  Human ALDH1L1/FTHFD
                                                                                                                                                                                                                                                                                26-JUN-2003
                                                                                                                                                                                                                                                                                                                                                ABZ46527 standard;
                                                                                   variation
                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 CAGGAGCACGTTCAGAAAGTTGCTGAAGTTTGTGG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                36
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                                                                 Location/Qualifiers replace(20. .21,CCT)/*tag= a
                                                                                                                                                                                                                                                                                                                                                DNA;
                                                                                                                                                                                                                                               gene polymorphic site, #3311.
                                                                                                                                                                                                                                                                                entry
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Pred. No. 1.8e
0; Mismatches
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WO200252044-A2

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RESULT 11
AAX19312
                                                                                                                                                                                                                                                                                                                                          Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes ce encoding enzymes associated with drug metabolism. The invention relates to methods and compositions for identifying individuals who have at least cone polymorphism in such drug metabolising enzyme-encoding genes. The complymorphism may be identified in a nucleic acid sample using probes or primers specific for a sequence selected from ABZ4217-ABZ50887 using a covariety of detection assays, including hybridisation assays, nucleic acid carrays and ecr-based methods. The invention also encompasses methods of cevaluating and screening drugs using genetic polymorphism data. Genetic polymorphism data, particularly that relating to single nucleotide polymorphism covariations and human diseases, conditions, and responses to that cause or exacerbate certain diseases, somethor genes could not be above respects as they are stable in populations, occur frequently, and have lower mutation rates than other genome variation of cour therapies based upon the genetic profile of individual patients. Cour the above respects as they are stable in populations, occur frist would not only take the guesswork out of selecting the drug with the correction and analysis of polymorphisms could the court of the invention are also useful in the drug discovery and greatest therapeutic effect for a particular patient, but would also creduce the likelihood of adverse reactions, thereby increasing safety. Complying the patient patient populations and respects of the invention are also useful in the drug discovery and sproval processes. For example, individuals could be selected for capabroyal trials only if their genetic profiles indicate that they are collinical trials only if their genetic profiles indicate that they are compositions of the invention and the selected for the inventions of the court of the compositions of the line patients are on medication and the number of different medications, failed drug trials, the time taken for a daverse drug to be approved. The cour
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SEXEXE
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                                                                                                                                                                                                                                                                 Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nakamura Y,
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02-MAY-2001; 2001JP-00135256
27-AUG-2001; 2001JP-00256862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 23; Page 119; 2785pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-DEC-2001;
                                                                                                                                                                                                                                                                                                                                        Sequence 40 BP; 6
                  17-MAY-1999
                                                                                           AAX19312 standard;
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                                                                                                                                                                                                                                                                                 Similarity
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                (first entry)
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                                                                                                                                                                                                                                                                                                                                          A; 15 C; 9 G;
                                                                                             DNA;
                                                                                                                                                                                                                                                                                 3.1%;
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                                                                                                                                                                                                                                                                               Score 20.6;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                          10
                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                          T; 0 U; 0 Other;
                                                                                                                                                                                                                                                         Db
1.8e+05;
9;
                                                                                                                                                                                                                            167
                                                                                                                                                                                                                                                                                                   Length 40;
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0.

Unidentified PCR primer; male Primer 172del-R.

sterile plant; RNAase inhibitor;

WO200124616-A1

12-SEP-2000; 2000WO-JP006222

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RESULT 12
AAF86438/c
ID AAF864
                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes the N-terminal peptide of human granulocyte colony-stimulating factor (hg-CSF). The present invention also describes: (1) recombinant plasmid pYHM-G-CSF containing the cDNA for the peptide; and (2) E. coli BI21 (pYHM-G-CSF) (KCTC 0477BP) transformed with the plasmid. The plasmid and E. coli strain are used to produce high yields of highly purified hG-CSF, which when refolded has comparable biological activity of G-CSF. hG-CSF is used to treat haematopoiesis disorders. The method of producing hG-CSF is less time-consuming and, therefore, more economical than previous methods because the protein is expressed in high yields without the need for further processing steps. AAX19290 to AAX19315 represent primer used in the synthesis of hG-CSF from an example of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human
                                        AAF86438;
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 41 BP; 4 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human granulocyte colony-stimulating factor (hG-CSF) containing a peptide at the N-terminus - useful in the treatment of haematopoiesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-MAY-1997;
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25-JUN-2001
                                                                                      AAF86438 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG. (JEIL-) JEIL PHARM CO LTD.
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                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           granulocyte colony-stimulating factor; G-CSF; hG-CSF;
                                                                                                                                                                                                                                                                                            26;
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                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                              Conservative
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(first entry)
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                                                                                      DNA;
                                                                                                                                                                                                                                                                                                               3.1%;
74.3%;
                                                                                                                                                                                                                                                                                                                                                                                   12 C; 13 G; 12 T; 0 U; 0 Other;
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                                                                                         42
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                                                                                                                                                                                                                                                                                         ,
                                                                                                                                                                                                                                                                                         Score 20.6; D
Pred. No. 1.8e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                  .8e+05
                                                                                                                                                                                                                                                                                                                                            B
                                                                                                                                                                                                        36
                                                                                                                                                                                                                                                                                                                                       Length 41;
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                                                                                                                                                                                                                                                                                              Gaps
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30-SEP-1999;

99JP-00279307

nucleic

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RESULT 13
ABZ48702
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Identifying individuals having a polymorphism, useful for determining the effectiveness or side effect of a drug or treatment protocol, comprises detecting at least one polymorphism in the drug metabolizing enzyme
                                                                                                                                                                                                                                                                  27-DEC-2000; 2000JP-00399443.
02-MAY-2001; 2001JP-00135256.
27-AUG-2001; 2001JP-00256862.
                                                                                                                                                                                                                                                                                                                                                                              27-DEC-2001; 2001WO-JP011592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polymorphic site; drug evaluation; drug screening; genotyping; genetic profiling; therapeutic customisation; adverse reaction; clinical trial; drug approval; single nucleotide polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; drug metabolising enzyme; gene; drug metabolism; chromosome 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human N-methyltransferase PEMT gene polymorphic site, #5485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABZ48702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene and inserting it into the plant genome. The method is u producing male sterile tobacco, lettuce and rapeseed plants, preferably rice and maize. The present sequence is a PCR prince
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ferably rice and maize. The presentinvention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention relates to a method for producing male sterile nts. The method comprises inserting a promoter fragment upstream se gene and a second promoter, upstream of an RNAse inhibitor prosecutions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens
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                                                                                                                                                               Sekine
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/*tag= a
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RESULT 14
ABZ43362
ID ABZ43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cc evaluating and screening drugs using genetic polymorphism data. Genetic cc polymorphism data, particularly that relating to single nucleotide cc polymorphisms (SNPs), may be used in studying the relationship between CC DNA sequence variations and human diseases, conditions, and responses to drugs. SNPs are also useful as polymorphism markers for discovering genes that cause or exacerbate certain diseases. SNPs are particularly useful in the above respects as they are stable in populations, occur frequently, and have lower mutation rates than other genome variations of cc such as repeating sequences. The detection and analysis of polymorphisms cc in genes encoding drug metabolising enzymes allows the customisation of creduce the likelihood of adverse reactions, the customisation of creduce the likelihood of faverse reactions, thereby increasing safety. Cc methods of the invention are also useful in the drug discovery and capable of responding to a particular profiles indicate that they are capable of responding to a particular drug orders that they are capable of responding to a particular drug orders that they are capable drug canadates could be revived if they were matched with more appropriate patient populations. The methods, data and compositions of the invention may therefore lead to a an increase in the range of consiste of time patient are on medication and the number of different medications, a patient needs to take before finding an effective therapy consisted the patient needs to take before finding an effective therapy.
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                                                                                                                                                                                                                                                                                                                                Human; drug metabolising enzyme; gene; drug metabolism; chromosome 17; polymorphic site; drug evaluation; drug screening; genotyping; genetyping; therapeutic oustomisation; adverse reaction; clinical trial; drug approval; single nucleotide polymorphism; SNP; ds
                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                     variation
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                                                                                                                                  Location/Qualifiers replace(21,T)
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WO200252044-A2

- SEQ ID No 121

Human pigmentation trait-related PCR primer

04-JUL-2002

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339 TCCAGGAGCTCTGCATCCCCCAAGACCTGGTCGGGG 374
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ID ABT34022 standard; DNA; 45
                                                                                                                                                                                      Best Local Similarity
Matches 26; Conserv
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                               Nakamura Y,
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Human, single nucleotide polymorphism; SNP; ss; melanocortin-1 receptor genetic pigmentation trait; MClR; agouti signaling protein; ASIP; race; hair colour; eye colour; forensic tool; PCR; primer.
                                                                                                                                                                                                                                                                                                                                                                                                                     21-UUN-2001, 2001US-0300187P.
07-AUG-2001, 2001US-0310781P.
17-SEP-2001, 2001US-0323662P.
26-OCT-2001, 2001US-0344418P.
15-NOV-2001, 2001US-0334674P.
02-UNN-2002, 2002US-034630P.
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequences ABZ43217-ABZE0887 represent polymorphic sites within genes encoding enzymes associated with drug metabolism. The invention relates conceding and compositions for identifying individuals who have at least con polymorphisms in such drug metabolising enzyme-encoding genes. The cone polymorphisms may be identified in a nucleic acid sample using probes or polymorphisms may be identified in a nucleic acid sample using probes or variety of detection assays, including Mybridisation assays, nucleic acid sample using probes or variety of detection assays, including Mybridisation assays, nucleic acid sample using probes or variety of detection assays, including Mybridisation assays, nucleic acid sample using probes or variety of detection and the invention also encompasses methods of evaluating and screening drugs using genetic polymorphism data, particularly that relating to single nucleotide oplymorphism (SMPs), may be used in studying the relationship between polymorphism (SMPs), may be used in studying the relationship between contags. SNPs are also useful as polymorphism markers for discovering genes that cause or exacerable certain diseases. SNPs are particularly useful in the above respects as they are stable in populations, occur frequently, and have lower mutation rates than other genome variations from a sequence. The genesic profile of individual patients.

Contage therapies based upon the geneticn profile of individual patients.

Contage therapeutic effect for a particular patient, but would also greatest therapeutic effect for a particular patient, but would also contage therapeutic of adverse reactions, thereby increasing safety.

Contage the patient populations. The methods of the invention may therefore lead to a nincrease in the range of the invention may therefore lead to a an increase in the range of the invention may therefore lead to a an increase in the range of the invention may therefore lead to a an increase in the range of the length of time patients are on medication and the medication
                                                                                                                                                                                                                                                                                                                                                                       Identifying individuals having a polymorphism, useful for determining effectiveness or side effect of a drug or treatment protocol, comprise detecting at least one polymorphism in the drug metabolizing enzyme
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                                                                                                                                                                                                                                                                         Saito S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 23; Page 66; 2785pp; English.
                                                                                                                                                                                                                                                                         lida A,
                                                                                                            27-DEC-2000; 2000JP-00399443.
02-MAY-2001; 2001JP-00135256.
27-AUG-2001; 2001JP-00256862.
                                                              27-DEC-2001; 2001WO-JP011592.
                                                                                                                                                                                                                                                                         Sekine A,
                                                                                                                                                                                                                                                                                                                            WPI; 2002-583571/62.
                                                                                                                                                                                                                        (RIKE ) RIKEN KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
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Inferring genetic pigmentation trait such as hair/eye color or shade from nupleic acid sample of human subject, by identifying a pigmentation-related haplotype allele of a pigmentation gene in the sample.

DNAP-) DNAPRINT GENOMICS INC

WPI; 2003-239091/23.

nucleic

Frudakis T;

28-MAY-2002; 2002WO-US016789

WO200297047-A2.

35-DEC-2002

Homo sapiens.

2001US-0293560P

25-MAY-2001;

Example 17; Page 245; 396pp; English.

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The invention comprises a method for inferring a genetic pigmentation trait of a human. The method involves identifying a single nucleotide polymorphism (SMP) in a pigmentation gene — where the pigmentation gene is not melanocortin-1 receptor (MCIR) and agouti signaling protein (ASIP). The method of the invention is useful for inferring a genetic pigmentation trait of a human, especially for inferring a genetic human subject. The method is useful for inferring a genetic pigmentation trait of a human, especially for inferring a genetic pigmentation trait such as hair shade or colour, or eye shade or colour of a human subject. The method may be useful as a forensic tool for obtaining information relating to physical characteristics of a potential crime victim or a perpetrator of a crime from a nucleic acid sample present at a crime scene. The present PCR primer is used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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Pred. No. 2.5e+05;
0; Mismatches 10; Indels
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Job time : 308.726 secs
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Best Local Similarity 72.2%;
Matches 26; Conservative
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Gaps ö

(first entry)

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Sequence 808, Application US/09671317

GENERAL INFORMATION:

APPLICANT: Chumakov, Ilya

FILE REFERENCE: 62.US3.CIP

CURRENT FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: US 60/536,178

PRIOR APPLICATION NUMBER: US 60/126,269

PRIOR FILING DATE: 1999-03-25

PRIOR PILING DATE: 1999-04-30

PRIOR FILING DATE: 1999-04-30

NUMBER OF SEQ ID NOS: 977

SOFTWARE: Patent.pm

SOFTWARE: Patent.pm
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1 LOCATION: 24

2 CIHER INFORMATION: 12-132-437 : polymorphic base A or

US-09-671-31-808
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Pred. No. 2.3e+03;
1; Mismatches 14;
US-08-176-412-5
US-08-555-568A-5
US-08-555-568A-5
US-08-123-95-5
US-08-123-936-74
US-08-123-936-74
US-08-123-936-74
US-09-354-947-74
US-09-671-317-78
US-09-671-317-78
US-09-671-317-839
US-09-671-317-839
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US-09-671-317-839
US-09-671-317-839
US-09-674-1159
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Patent No. 6528260
GENERAL INFORMATION: APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
APPLICANT: Bougueleret, Lydie
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hes 29; Conserv
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US-09-671-317-639
     LENGTH: 47
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22, Appl
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Sequence 2, Appli
                                                                                                                                                                February 29, 2004, 11:48:29; Search time 67.9494 Seconds (without alignments) 5488.301, Million cell updates/sec
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1 atgtctgctttgggggctgc.....gtgagcgcaaactgcaggac 672
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
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Compugen Ltd.
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US-08-173-396-463

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US-08-482-080A-463

US-09-354-947-463

US-09-354-947-463

US-09-252-222

US-09-252-222

US-09-252-228-80

US-09-422-978-2676

US-09-422-978-2676

US-09-422-978-2676

US-09-422-978-2676

US-09-422-978-2676

US-09-422-978-2676

US-09-252-098-80

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US-09-292-069A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                               682709 segs, 277475446 residues
                                GenCore version (c) 1993 - 2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                        using sw model
                                                                                                                                                                                                                                                               US-09-904-568-1_COPY_132_
                                                                                                                                                                                                                                                                                                                                                           IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Match Length
                                                                                                                        nucleic search,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 50
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                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number
                                                                                                                          nucleic
                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database
                                                                                                                                                                     Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 259 GCGGGCACACACACCTCCAGCAGGCTCTCCGGCTGCCCCC 302
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3.0%; Score 20; DB 1; Length 50;
Best Local Similarity 65.9%; Pred. No. 5.5e+03;
Matches 29; Conservative 0; Mismatches 15; Indels
                                                                                                          APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49 ccececcaceccicecicinaracinoscocicacios e con esta e con e con esta e con esta e con esta e con en esta e con esta e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4600-0175/G19P3
                                                                                                                                                                                                                                                                                                                                                                                            E: Genelabs Technologies, Inc.
505 Penobscot Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR PAPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNES APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNES APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNES APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNES FABLAIN. GATY R.
REGISTRATION NUMBER: 33,875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 463, Application US/08123936
Patent No. 5726014
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 460C
TELECOMMUNICATION INFORMATION:
TELEFONE: (415) 324-080
TELEFAX: (415) 324-080
INFORMATION FOR SEQ ID NO: 463:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 50 base pairs
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INDIVIDUAL ISOLATE: INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Redwood City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: C.
                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: TANABE SEIYAKU CO. LTD.
APPLICANT: TANABE SEIYAKU CO. LTD.
APPLICANT: TANABE SEIYAKU CO. LTD.
APPLICANT: TANAGUCH, Tomoyasu
APPLICANT: TANGUCH, Tomoyasu
APPLICANT: MIZUKAMI Junko
TITLE OF INVANTION: METHOD FOR IDENTIFYING OR SCREENING AGONIST AND ANTAGONIST TO PPA
FILE REFERRNCE: TANIGUCHI=6
CURRENT APPLICATION NUMBER: US/09/514,247A
CURRENT FILING DATE: 1998-08-24
PRIOR FILING DATE: 1998-08-24
PRIOR FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 10
SSOFTWARR: Patentin version 3.0
SEQ ID NO 2
LENGTH: 35
                     TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM FILE REFERENCE: 62.US3.CIP
FILE REFERENCE: 62.US3.CIP
CURRENT APPLICATION NUMBER: 2000-09.27
PRIOR APPLICATION NUMBER: 2000-03.23
PRIOR PLING DATE: 2000-03.24
PRIOR FILING DATE: 2000-03.24
PRIOR FILING DATE: 1999-03.25
PRIOR FILING DATE: 1999-04.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) OTHER INFORMATION: Artificially synthesized primer sequence US-09-514-247A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     596 AGCTGCGGTACAGTGTAGCCTTGGTCCTTAAGGAGATGGCAGAAC 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: allele
LOCATION: 24
COTHER INFORMATION: 10-260-282 : polymorphic base G or US-09-671-317-639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 20.6; DB 4;
Pred. No. 3.5e+03;
1; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86 CCTCTCCAGAAGTGACGGCCGTGGCTCAGCTCT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ccecrceadaarerreceadrecercadeacr 33
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; Sequence 463, Application US/08171389
; Patent No. 5578444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09514247A
Patent No. 6365361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 75.8°
Matches 25, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
Cohen, Annick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 29; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 639
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US-08-482-080A-463/c
; Sequence 463, Application US/08482080A
; Patent No. 6010849
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                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGIA : DO MOLECULE TYPE: DN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
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APPLICANT: Turin, Lisa M.

TITLE OF INVENTION: Screening Assay for the Detection of TITLE OF INVENTION: BNA-Binding Molecules
NUMBER OF SEQUENCES: 640
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STAME: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INDIVIDUAL ISOLATE: Human insulin-like growth factor II INDIVIDUAL ISOLATE: gene
US-08-123-936-463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                259 GCGGGCACACACACCCTGCTCCAGCAGGCTCTCCGGCTGCCCCC 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 20; DB 1; Length 50; Pred. No. 5.5e+03; 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cancor, Charles R.
APPLICANT: Cancor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 664
ADDRESSEE: Genelabs Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49 GCGGGCCCACGCCCCGGCTCTTATAGTCGCGCCAGCCGCGGCC 6
                                                                                                                                                                          NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REGISTRATION NUMBER: 4600-0075,32/G19P2
TELEPHONE: (415) 324-0860
TELEPHONE: (415) 324-0960
INFORMATION FOR SEQ ID NO: 463:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 463, Application US/08475228A Patent No. 5869241
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 65.9
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 50 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
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US-08-475-228A-463/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
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Gaps
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APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF SEQUENCES: 664
CORRESPONDENCES: 664
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INDIVIDUAL ISOLATE: Human insulin-like growth factor II INDIVIDUAL ISOLATE: gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 50;
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COMPUTER KEALALALE FORM:
MEDIUW TYPE: FIDOPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin Nomer: US/08/475,228A
PRICHATION NOMER: US/08/475,228A
PRICHATION NOMER: US/08/475,228A
PRICHATION NOMER: US/08/475,228A
PRICHATION NOMER: US/08/123,936
PRICHATION NOMER: US/07/996,783
PRICHATION NOMER: US/07/996,783
PRICHATION NOMER: US/07/996,783
PRICHATION NOMER: US/07/23,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNET/ANDER
NAME: Stratford, Carol A.
REGITEATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 4600-0175.21/G19F3D2
TELECOMOUNICATION INFORMATION:
TELEFRAX: (415) 324-0860
TELEFRAX: (415) 324-0860
TELEFRAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 463:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 3.0%; Score 20; DB 2; I Best Local Similarity 65.9%; Pred. No. 5.5e+03; Matches 29; Conservative 0; Mismatches 15.
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PCT-US93-12388-463/C
Sequence 463, Application PC/TUS9312388
GENERAL INFORMATION:
JAPPLICANT:
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
JUNBER OF SEQUENCES: 641
CORRESPONDENCES: 641
CORRESPONDENCES: Genelabs Technologies, Inc.
STREET: 505 Pennobscot Drive
CITY: Redwood City
STREET: 505 Pennobscot Drive
CITY: Redwood City
STREET: 506 Pennobscot Drive
STREET: 507 Pennobscot Drive
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BALDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INDIVIDUAL ISOLATE: Human insulin-like growth factor II INDIVIDUAL ISOLATE: gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.0%; Score 20; DB 4; Length 50; 65.9%; Pred. No. 5.5e+03; tive 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       259 GCGGGCACACACACCCTGCTCCAGCAGGCTCTCCGGCTGCCCCC 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 ecededececedececececentrariales de decedececente 6
                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATE: 20-1993

PRIOR APPLICATION DATE: 20-1993

PRIOR APPLICATION NUMBER: US 08/123,936

FILING DATE: 17-SEP-1993

PRIOR APPLICATION NUMBER: US 07/996,783

PRIOR APPLICATION DATE: 23-DEC-1992

PRIOR APPLICATION DATE: 23-DEC-1992

PRIOR APPLICATION DATE: 27-UDN-1991

PRIOR APPLICATION DATE: 22-UDN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Brady, John F.

REGISTRANCHON NUMBER: 4600-0175.20/G19P3D1

TELEPONEY: (650) 324-0880

TELEPONEY: (650) 324-0880

TELEPONEY: (650) 324-0860

TELEPONEY: (650) 324-0860
                                                          OPERATURA SIGLARIA FULLOS NOTATION #1.25
SOUTHARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/354,947
FILING DATE: US 08/482,080
FILING APPLICATION NUMBER: US 08/482,080
FILING DATE: 07-UN-1995
FILING DATE: 20-DEC-1993
FILING DATE: 20-DEC-1993
    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 65.9
Matches 29, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
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Patent No. 6384208
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF ENVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESS: Genelabs Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INDIVIDUAL ISOLATE: Human insulin-like growth factor II
INDIVIDUAL ISOLATE: gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          259 GCGGGCACACACCCTGCTCCAGCAGGCTCTCCGGCTGCCCCC 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.0%; Score 20; DB 3; Length 50;
65.9%; Pred. No. 5.5e+03;
live 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 geggegecekececegererrarkaresececeeeee
                                                                                                   COFFAILNES STSIEM:
CURRENT APPLICATION NUMBER:
PALORATION NUMBER:
PRICATION APPLICATION NUMBER:
PRICATION DATE:
PRICATION NUMBER:
PRICATIO
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (650) 324-0960 INFORMATION FOR SEQ ID NO: 4 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.09
Best Local Similarity 65.99
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            i. 50 base pairs
nucleic acid
EDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
US-09-354-947-463/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-482-080A-463
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Gaps .. 0

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GENERAL INFORMATION:
APPLICANT: Flor, Peter J.
APPLICANT: Flor, Peter J.
APPLICANT: Flor, Feter J.
APPLICANT: Lindaur, Kristen
APPLICANT: Lindaur, Kristen
APPLICANT: Lindaur, Kristen
APPLICANT: Lindaur, Kristen
APPLICANT: Morpfel, Thomas
TITLE OF INVENTION: Hume, HmR7, and Related DNA Compounds
TITLE OF INVENTION: HmR6, HmR7) and Related DNA Compounds
FILE REFERENCE: 4-19679/A/PCT
CURRENT APPLICATION NUMBER: US/08/617,464
CURRENT RILING DATE: 1096-03-19
EARLIER APPLICATION NUMBER: BPO 9416553.7
EARLIER PELING DATE: 1994-08-19
EARLIER PILING DATE: 1994-08-19
EARLIER PILING DATE: 1993-09-20
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 19
                                                                                  APPLICANT: Flor, Peter J.
APPLICANT: Kuhn, Raniez
APPLICANT: Kuhn, Raniez
APPLICANT: Kuhn, Raniez
APPLICANT: Min, Raniez
APPLICANT: Min, Raniez
APPLICANT: Monas
ITELE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4, ITELE OF INVENTION: HMR6, HMR7) and Related DNA Compounds
ITILE OF INVENTION: HMR6, HMR7) and Related DNA Compounds
ITILE OF INVENTION: HMR6, HMR7) and Related DNA Compounds
CURRENT APPLICATION NUMBER: US/08/617,785E
CURRENT FILING DATE: 1996-03-19
EARLIER FILING DATE: 1994-09-07
EARLIER FILING DATE: 1994-09-07
EARLIER FILING DATE: 1994-09-07
EARLIER FILING DATE: 1993-09-07
EARLIER FILING DATE: 1993-09-07
EARLIER FILING DATE: 1993-09-07
EARLIER FILING DATE: 1993-09-07
EARLIER PILING DATE: 1993-09-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: Oligonucleotide primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 266 CACACACCTGCTCCAGCAGGCTCTCCGGCTGCCCCTGC 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
2.9%; Score 19.2; DB 3; 1
Best Local Similarity 67.5%; Pred. No. 9.2e+03;
Matches 27; Conservative 0; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42 cccacrccrascccrascascascarecescascas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oligonucleotide primer
   Sequence 19, Application US/08617785E
Patent No. 6228610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19, Application US/09817464
Patent No. 6515107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION:

) OTHER INFORMATION:

US-09-817-464-19
                                                               GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Boudec, Phillipe
APPLICANT: Boudes, Matthew
APPLICANT: Boudes, Matthew
APPLICANT: Rodgers, Matthew
TITLE OF INVENTION: Mutaced hydroxyphenylpyruvate dioxygenase, DNA
TITLE OF INVENTION: sequence and isolation of plants which contain such a
TITLE OF INVENTION: sequence and isolation of plants which contain such a
TITLE OF INVENTION: gene and which are tolerant to herbicides
FILE REFERENCE: 5500*31
CURRENT APPLICATION NUMBER: US/09/252,292B
CURRENT APPLICATION NUMBER: US 08/982,772
PRIOR PAPLICATION NUMBER: US 08/982,772
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human insulin-like growth factor II gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.0%; Score 20; DB 5; Length 50;
65.9%; Pred. No. 5.5e+03;
tive 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49 GCGGGCCCACGCCCCCTCTTATAGTCGCGCCAGCCGCGCC 6
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                                            CLASSIPICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
SPELICATION NUMBER:
BRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
PILING DATE: 23-DEC-1992
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0175.41/G19PCT2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 463:
SEQUENCE CHARACTERISTICS:
LENGTH: SO Dasse pairs
TVDE:
LENGTH: SO Dasse pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42
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PCT/US93/12388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 22, Application US/09252292B
Patent No. 624596B
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 65.9
Matches 29; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INDIVIDUAL ISOLATE: INDIVIDUAL ISOLATE:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Plant
US-09-252-292-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT-US93-12388-463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-252-292-22
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Matches
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Length 44;

Score 19.2; DB 4; Pred. No. 9.2e+03;

2.9%;

Query Match Best Local Similarity

RESULT 11 US-08-617-785-19/c

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Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,928
FILING DATE: 05-Jan.1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 19; DB 2; 
Pred. No. 8.3e+03; 
0; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                 ); OTHER INFORMATION: oligonuclectide primer US-08-859-998-80
                                                                       REGISTRATION NUMBER: 37,620
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELEPHONE: 415-322-5070
ITELEPRX: 415-854-0875
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/859,998
FILING DATE: 21-MAY-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43 GCTGACAGTCACAGTGGCCGGGTCAGT 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Elbilashvilli, Rober
Elille OF INVENTION: EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 80, Application US/09225928
Patent No. 6352829
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 415-322-5070
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Jokhadze, George
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INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.8%;
Best Local Similarity 81.5%;
Matches 22; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diske
                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: DNA
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APPLICANT: Cohen, Daniel
APPLICANT: Cohen, Daniel
APPLICANT: Chumakov, ilya
in Interest and in Constructing a high density...
FILE REPERSHYCE: GENET COCOPT
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT APPLICATION NUMBER: US 09/298,850
EARLIER APPLICATION NUMBER: US 60/109,732
BARLIER FILING DATE: 1999-04-21
BARLIER FILING DATE: 1999-04-21
BARLIER FILING DATE: 1998-04-21
BARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
LENGIH: 47
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  Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: 99-13864-64 : polymorphic base G or T
US-09-422-978-2676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASSAYING DIFFERENTIAL
                                                                                    Score 19.2; DB 4;
Pred. No. 9.5e+03;
1; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,998
FILING DATE: 21-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Fish & Richardson, P.C. STREET: 2200 Sand Hill Road, Suite 100 CITY: Menlo Park STATE: QE COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Chenchik, Alex
APPLICANT: Jokhadze, George
APPLICANT: Jokhadze, George
TITLE OF INVENTION: METHOD OF ASSA
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
                                                                                                                                                                              ce 2676, Application US/09422978
No. 6537751
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Best Local Similarity 70.6
Matches 24; Conservative
    27; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo Sapiens
                                              266 CACACACCCTG
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LOCATION: 24
    Matches
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COTHER INFORMATION: oligonuclectide primer
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SEQUENCE DESCRIPTION: SEQ ID NO: 80;
US-09-225-928-80

Query Match
Query Match
Best Local Similarity 81.5%; Pred. No. 8.3e+03;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps
Qy 43 GCTGACACTCACAGGGGGGCAC 69

Db 27 GCAGACACTCACAGGTTTGGTCGF 1
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Search completed: February 29, 2004, 14:42:39 Job time : 70.9494 secs

Human gen Human Akt 3' PCR pr Human Akt

Abq82800 Abv76886

Human Akt Human Akt Human Akt Primer #4 Primer #4

Abq82813 | Aba00519 | Aad47158 |

Reverse P PCR prime Human SNP

Human Human

Aav90578 BAbk96448 BAal29231 BAbz01371 BAbz01372 Abz01296 BAbz01296 BAbk65992

Human pro Human SNP L-galacto Maize pol Human CG0

Aba98210 Abk52805 Aal30792 Aat61009 Aav51259 Aad02645

Ade06642 Ade15856 Add96154

Oligonucl

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Prodrug, TNF; tumour necrosis factor; selectokine; chimeric; W24; W33; cytostatic; immunomodulatory; antiangiogenic; apoptosis inducer; gene therapy; scFv antibody OS4; fibroblast activation protein; tenascin; solid tumour; angiogenesis; treatment; infection; metabolic disease; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel polypeptide (1) comprising, in the N to C direction, a region (R1) that recognises selectively a specific macromolecule on a cell surface and/or a component of the extracellular matrix, peptide linker, a region (R2) with biological activity for a specific target molecule, a region (R3) that has a processing site and region (R4) that inhibits the activity of R2, by intramolecular bonding and/or interaction. The products of the invention have cytostatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptide prodrug, useful e.g. for treating tumors, c
targeting region, active agent and attached inhibitor that
proteolytically cleaved in target cells.
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                    AAV90578
ABK96448
                                      AAL29231
ABZ01371
ABZ619371
ABX65990
ABQ82800
ABQ82813
ABA00513
AAD47158
ADD6654
ADD6654
ADB66642
ADB78866
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ABA99919/c
ID ABA99919 standard; DNA; 49 BP.
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PFIZENMAIER K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         primer; as.
ABA99919;
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(PFIZ/)
472222EEEEEEEEEEE EEE 44444
47967866666666664444444
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Aba24835 Herpes Si
Aba71444 Human meg
Ab14038 Primer 3
Aat89030 Solid pha
Aa45886 Cytomegal
Aa460503 Hepatoma
Aax27881 PPAR CDNA
Aai66427 Kringle p
Aaq22113 53 chimer
Aa13495 Human ins
Aa466713 Human ins
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S3 chimer
Human SNP
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Human map
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Human HNK
Human HNK
Human ATP
                                                                      2004, 09:53:57; Search time 303.274 Seconds (without alignments) 9413.223 Million cell updates/sec
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Compugen Ltd.
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          version :
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Maximum Match 100%
Listing first 45 summaries
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ABK82954
ABZ00686
ADE80493
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ABZ43700
ABZ49884
ABV75966
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ABL40388
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Gapop 10.0 , Gapext 1.0
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geneseqn2002s:*
geneseqn2003as:*
geneseqn2003cs:*
geneseqn2004s:*
            GenCore (c) 1993
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Match Length
                                                     nucleic search,
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seq length: 50
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contains

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Scheurich P;

allow sensitive and correct determination of sex hormonal activity. The present sequence is a PCR primer, which was used in an example from the

Sequence 50 BP; 7 A; 12 C; 18 G; 13 T; 0 U; 0 Other;

invention

88988

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Gaps

; 0

16; Indels Length

DB 7;

Score 21.4; DB 7; Pred. No. 3.4e+04; 0; Mismatches 16

3.2%; Local Similarity 66.0%; Les 31; Conservative

Query Match

Best Loca Matches

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used for gene therapy. Kym-1 cells (2000) were incubated with the product W24, containing, essentially, the single-chain Fv antibody 054, predity for the human tibroblast activation protein, trimerization linker, mutant form of the tumour necrosis factor (TNF) precursor protein, a region with a proteolytic cleavage site, and human TMP receptor-1 fragment, and with trypsin (activator) for 5 minutes. After 16 hours, cell viability was determined by MTT staining. Activated W24 had LD50 about 0.5 mg/m1, comparable with that for wild-type TMF and 4000 times higher than for uncleaved W24. [1], also nucleic acids encoding them and related vectors, are useful particularly for treating solid tumours and metabolic diseases. [1] are producy forms of R2 that have neceptable toxicity when administered systemically (specifically tumour neceptable toxicity when administered systemically (specifically with retention of, or even increase in, therapeutic activity. R2 is released only in target tissue, resulting in a high local concentration, and activity is potentiated by co-activation of the human TMF fragment is used in the construction of the TMF selectorium of the human TMF fragment of the TMF selectorium of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to cells obtained by introduction of a reporter expression nucleic acid, which comprises a response element and a promoter downstream of the response element. The promoter controls transcription in animal host cells to significantly stimulate the expression of the reporter gene in the presence of a ligand bound to an intranuclear receptor. The cells are used for evaluation of a sex hormone receptor e.g. androgen receptor (AR) and oestrogen receptor (ER) and
immunomodulatory and antiangiogenic activity, induce apoptosis and can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cells for evaluation of agonistic and antagonistic activities to a nuclear receptor of a substance, comprise a stable expression cell line of an intranuclear receptor gene and a reporter gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.2%; Score 21.8; DB 6; Length 49; 1 Similarity 70.7%; Pred. No. 2.6e+04; Length 49; 29; Conservative 0; Mismarth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR; primer; intranuclear receptor; sex hormone receptor; androgen receptor; AR; oestrogen receptor; ER; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Herpes Simplex Virus thymidine kinase PCR primer TK3'-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 TGGGTTCCCAGCCCTCTCCAGAAGTGACGGCCGTGGCTCAG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 49 BP; 12 A; 15 C; 12 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     described in the disclosure of the invention
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Best Local Similarity
Matches 29; Conserv
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ABZ24835
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel DNA sequence (I) representing a promoter
                                                                                                                                                                                                                PCR primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA for promoter region of megsin useful for screening proteins.
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136 AGCACCTTCAGAAAGTTGTTGAAACTTGTAGTCGGGCCCCTGCATGG 182
                           4 Accrrciececacecrererrancecrerranecececreerecade 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 13.1%; Score 21; DB 3; Length 30; Local Similarity 82.8%; Pred. No. 3.7e+04; les 24; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                Promoter; megsin; human; protein isolation; screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 30 BP; 6 A; 10 C; 5 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                    Human megsin promoter PCR primer SEQ ID NO: 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135 GAGCACCITCAGAAGTIGITGAAACTIG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGCAGCTTCAGATAGGAGCTGAAACTTG 2
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                                                                                                  AAA71444 standard; DNA; 30 BP
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                                                                                                                                                                                                                                                                                                                                                             99JP-00015667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL40388 standard; cDNA; 33
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                                                                                                                                                                                                                                                                                                                                                                                       (KURO/) KUROKAWA K.
(MIYA/) MIYATA T.
                                                                                                                                                                                                                                                                          WO200043528-A1
                                                                                                                                                                                                                                                                                                                                                            25-JAN-1999;
                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                              AAA71444;
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ABL40388/c
ID ABL403
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AC ABL403
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ID AAÀ7
XX
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The present sequence represents a DNA probe which is used to demonstrate a new method for the detection of genes, using a synthetic gene in the solid phase. The gene has a (substituted) trityl group which binds to a hydrophobic carrier through an end protective group. The method is simple and the solid phased gene is stable. Gene amplification was carried out using a primer set to contain a point mutation determining each antigen type in the amplification region for HPA-1 to HPA-6. A synthetic DNA was prepared and a probe was immobilised on the plate. The present probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNA, enzyme; enzymatic RNA molecule, ERM, cleave; RNA; mRNA; HnRNA, picornavirus, HIV; immunodeficiency virus, hepatitis B virus; HBV; papilloma virus; HPV; Epstein-Barr virus; EBV; TCLV; T-cell leukaemia virus; hepatitis C virus; HCV, cytomegalovirus; influenza virus; HSV; herpes simplex virus; vector; immune response; antibody; ribozyme; viral RNA; treatment; ss.
                                                                                                                                                                                                        Solid phase gene - useful for detection of genes in a sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 21; DB 2; Length 40;
Pred. No. 4.1e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 40 BP; 7 A; 9 C; 11 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               308 GICTAAAGCCAGAIGCCTICCAGGAAGAGCICCAGGA 344
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                                                                                                                                                                                                                                                                     Example 1; Page 9; 12pp; Japanese.
                                                                                     (SUMQ ) SUMITOMO METAL IND LTD
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92US-00882712.
92US-00882713.
92US-00882823.
92US-00882886.
92US-00882886.
92US-00882886.
92US-00882889.
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92US-00882889.
92US-0088289.
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(first entry)
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                                                                                                                                               WPI:, 1997-540228/50
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14-MAY-1992;
14-MAY-1992;
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26-MAY-1994
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4-MAY-1992
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4-MAY-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ52858;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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AAQ52858
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polypeptide-HOMO phosphoryl transport protein 12 and encoding bolymucleotide, used in diagnosis and treatment of malignant tumors, hemopathy, human immunodeficiency virus infection, immunological diseases and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated polypeptide of polypeptide-HOMO phosphoryl transport protein 12. The activity of the polypeptide of the invention may be described as, cytostatic, haemostatic, virucide, immunomodulatory and antiinflammatory. Polypeptides and polymucleotides of the invention are used in diagnosis and treatment of malignant tumour, haemopathy, human immunodeficiency virus (HTV) infection; immunological diseases various inflammations, and phlospesses (HTV) infection, immunological diseases various inflammations, and phlospesses (HTV) infection; understand pene therapy. The current sequence represents a primer relative to the HOMO phosphoryl transport protein 12 of the invention
                                                                                                            HOMO phosphoryl transport protein 12; cancer; haemopathy; phlogosis; immune disease; HIV; human immunodeficiency virus; cytostatic; haemostatic; virucide; immunomodulatory; attiinflammatory; inflammation; gene therapy; malignant tumour; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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0
                                                            Primer 3 relative to HOMO phosphoryl transport protein 12.
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hydrophobic carrier; PCR primer; detection probe; HPA; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 33 BP; 5 A; 9 C; 13 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 21; DB 6; I Pred. No. 3.8e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 4; Page 18; 37pp; Chinese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-MAY-2001; 2001WO-CN000792,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.1%;
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(first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                              WO200200698-A1
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                                                                                                                                                                                                                                                                     Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-FEB-1998
01-JUL-2002
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4-MAY-1

26-AUG-

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The present sequence represents a segment of the hepatoma AS-30D Type II hexokinase promoter region. Response elements (transcription factor sequence. AS-30D in this fragment may consists of all or part of the present sequence. AS-30D is a new isolated hexokinase II. The present DNA fragment is capable of regularing transcription of a downstream open reading frame and contains at least one response element. The present DNA fragment may be coupled to a reporter gene and used to screen for potential drugs that affect regulated transcribtion of tumour hexokinase iI. Alternatively it may be coupled to a toxic gene and used to treat with cancer. It may also be used in gene therapy to treat diabetes. The DNA fragment increases glycolysis in cells and express homologous or the proper of the DNA fragment are used in the method that contains a proper of the DNA fragment are used in the method to the proper of the DNA fragment are used in the method to the pNA fragment are used in the method to the pNA fragment are used in the method to the DNA fragment are used in the method to the DNA fragment are used in the method to the DNA fragment are used in the method to the DNA fragment are used in the method to the DNA fragment are used in the method to the DNA fragment are used in the method to the DNA fragment are used in the method the DNA fragment are used in the method to the DNA fragment are used in the method to the DNA fragment are used in the method to the DNA fragment are used in the method the DNA fragment are used in the method to the DNA fragment are used in the method to the DNA fragment are used in the method to the DNA fragment are used in the method to the DNA fragment are used in the method to the DNA fragment are used in the method to the DNA fragment are used in the method to the DNA fragment are used in the method the DNA fragment and the DNA fragment are used in the method the DNA fragment and the DNA fragment are used in the DNA fragment and the DNA fragment and the DNA fragment and the DNA fragment and 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to methods for identifying potential agonists or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPAR; reporter gene; CAT;
CBP; SRC-1; lacZ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for diagnosing a neoplasia that over-expresses hexokinase. The new response elements are active only in tumours, not in normal cells
                                                                                New transcription regulating fragments of hexokinase II DNA contg. response element - and methods for diagnosis or treatment of neoplthat over-express hexokinase II and for regulating glycolysis.
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Pred. No. 5e+04;
0; Mismatches 17; Indels
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5e+04;
17;
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transcriptional coupling factor; screening;
antidiabetic; antiobesity; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example; Page 24; 34pp; Japanese.
                                                                                                                                                                                     Claim 1; Fig 11; 104pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPAR cDNA amplifying primer 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-MAY-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 64.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequences (AAQ52824-Q52890) are pref. Cytomegalovirus target sequences for enzymatic RNA molecules. The RNA molecules are complementary to a substrate binding region in the specified gene target. They also have enzymatic activity, in that they specifically cleave RNA in the target. The ERMs interfere with viral replication and therefore have anti-viral properties. They can be used to attenuate viruses to be used in vaccines. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enzymatic RNA molecules - used to inhibit viral replication, infection and gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Response element; Z-DNA; neoplasia; hexokinase II; glycolysis; cancer; gene therapy; diabetes; tumour; rat; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                            Holecek JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatoma AS-30D Type II hexokinase promoter fragment from -118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
3.1%; Score 20.8; DB 2; Length 42;
Best Local Similarity 60.0%; Pred. No. 4.8e+04;
Matches 24; Conservative 4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 TGTGGAGCAACTTGGTGCCAGCGCCAACCTGTCAGAAGAG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ududdangaccuacdddccaucdccaagaducadaudad 41
                                                                                                                                                                                                                                                                                                                                                                                                                            Macejak DG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 42 BP; 9 A; 9 C; 17 G; 0 T; 7 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rempel A;
                                                                                                                                                                                                                                                                                                                                                                                                                            Dudycz LW, Mcswiggen JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 5; Fig 13; 287pp; English.
92US-00884333.
92US-00884431.
92US-00884431.
92US-00884521.
92US-00923738.
92US-00938854.
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                                                                                                                                                                                                              92US-00948359.
92US-00963322.
92US-00987129.
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                                                                                                                                                                                                                                                                                                                                                                          (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT80503 standard; DNA; 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYJO ) UNIV. JOHNS HOPKINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1993-386599/48.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9704104-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-OCT-1997
                                                                                                                                     31-JUL-1992
                                                                                                                                                                                                                                                                                                                     07-DEC-1992
                                                          4-MAY-1992
                                                                                                                                                                                                                 18-SEP-1992
                                                                                                            14-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                         Draper KG,
Mamone JA;
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RESULT 7

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S3 chimeric neurotrophic factor PCR primer 6.

10-JUN-1992

AAQ22113;

Polymerase chain reaction.

Homo sapiens.

WO9202620-A.

20-FEB-1992

AAQ22113 standard; DNA; 44 BP.

4AQ22113

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polypeptide-kringle protein 13 for treating diseases, such as, cancer and human immunodeficiency virus infection.
antagonists to peroxisome proliferator-activated receptor (PPAR). The method comprises contacting the compound to a test cell containing the genes for PPAR and a transcriptional coupling factor together with a reporter gene. The test cell used for screening is a yeast or other cell which contains (a) DNA encoding PPAR (especially PPAR-gamma of human origin); (b) DNA encoding a transcriptional coupling factor such as SRC-1; (c) a suitable reporter gene (such as lacZ or CAT). Contact with the candidate agonist /Antagonist induces changes in the ligand-dependent interaction between PPAR and the transcriptional coupling factor in the test cell which is reflected in the expression of the anticipants and antigonists to PPAR can be used as anticipabetic and antichemic expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kringle protein 13; cancer; HIV infection; gene therapy; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides the protein and coding sequences of kringle protein 13. The sequences can be used in the treatment of and HIV infection. The present sequence is a probe for the coding
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                                                                                                                                                                                                                                                                 3.0%; Score 20.2; DB 2; Length 35; 75.8%; Pred. No. 6.6e+04; Live 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 41 BP; 4 A; 12 C; 18 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                 Sequence 35 BP; 7 A; 9 C; 11 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                              antidiabetic and antiobesity agents respectively
                                                                                                                                                                                                                                                                                                                                       86 CCTCTCCAGAAGTGACGGCCGTGGGCTCAGCTCT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 7; Page 19(Disclosure); 31pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                   CCCCTCGAGAATGTTGCCAGTGGCTCAGGACT 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kringle protein 13 coding sequence probe #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                Local Similaricy
hes 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYFU-) UNIV FUDAN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mao Y, Xie Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Simi:
Matches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified
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                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                    Matches
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The sequence is that of an oligonucleotide used in the construction of chimeric neurotrophic factor S3, it represents primer 6 in the polymerase chain reaction used to produce the chimera. See also AAR21851-R21874 and

Sequence 44 BP; 14 A; 6 C; 17 G; 7 T; 0 U; 0 Other;

AAQ22081-Q22131

caused by trauma, surgery, ischaemia, infection, metabolic diseases, nutritional deficiency, etc.

Disclosure; Page 67; 114pp; English.

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Lindsay

Furth ME,

Souinto SP,

Ip N,

Suter U,

Shooter EM, S' Yancopoulo GD;

WPI; 1992-080074/10.

90US-00564929. 90US-00564929.

08-AUG-1990; 08-AUG-1990; (REGE-) REGENERON PHARM INC

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                                                                                                                                                                                                                                                                                                               Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; delucoprofective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; angiopoietin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinase; cytokine; interferon; interleukin; G-protein coupled receptor; thiosesterase; inflammation; multifactorial disease; autoimmune disease; infection;
                                   Gaps
                                   ö
 Length 44;
                               13; Indels
                                                                184 AAAGACTGCAGAGAGAAGCTGTGGAGCAACTTGGTGCCAGCGC 224
                                                                                              4 AAAGACGCAGTGGACATGTCGGGTAAGGAGGTGACAGTGC 44
3.0%; Score 20.2; DB 2;
8.3%; Pred. No. 7.2e+04;
                                 0; Mismatches
                                                                                                                                                                                                                                                                                   Human SNP oligonucleotide #7753.
                                                                                                                                                                                    ВP
                 68.38;
                                                                                                                                                                                   AAL34545 standard; DNA; 50
                                                                                                                                                                                                                                                                                                                                                                                                                                   nervous system disease; ss
                                                                                                                                                                                                                                                   (first entry)
                                 28; Conservative
                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200147944-A2
                                                                                                                                                                                                                                                   24-JAN-2002
                                                                                                                                                                                                                  AAL34545;
Query Match
                 Best Loca
Matches
                                                                                                                                                                 AAL34545
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Gaps

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246 GGCCGTCCTGCTGCCGGCCACACACACCCTGCTCCAGCAGG 286 GGCCGCTCTGTGGGGTGGCACTCAGCCGCTGCTGAAGCGGG 41

ò g

Conservative

Similarity

Fry KE

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of synthetic or biological cpds. for their ability to bind DNA test sequences. The assay is versatile in that any number of test sequences can be tested by placing the test sequence adjacent to a defined protein chinding screening sequence. Binding of mols. to these test sequences binding screening sequence. Binding of mols. to these test sequences changes the binding characteristics of the protein mol. to its cognate chinding sequence. When such a mol binds the test sequence, the equilibrium of the DNA:protein complexes is disturbed, generating changes in the concentration of free DNA probe. One application of this method is to eucaryotic general transcription factors (e.g. TFILD), where the target region is typically selected from DNA sequences adjacent to the binding site for the eucaryotic transcription factor. Numerous exemplary test sequences are given: the sequences in AAQ69251-711 and AAQ69850 correspond to promoter targets (typically, TATA box-contg. sites) for human genes and the sequences in AAQ69312-899 correspond to promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         targets for viral genes. The test sequences may also be randomly generated. DNA.protein interaction may be used for screening purposes, e.g. the Herpes Simplex Virus (HSV) origin of replication and UL9 (see AAQ69851-52, AAQ69865 and AAQ69891). (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Duplex DNA; target region; binding characteristic; DNA binding protein; TFIID; transcription factor; binding site; inhibition; enhance; cancer; inherited genetic disorder; ds.
                                                                                                                                                                                               Sequence-directed DNA-binding molecules - useful in pharmaceuticals and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human insulin-like growth factor-II gene TFIID binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 20; DB 2; Length 50;
Pred, No. 8.6e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       259 GCGGGCACACACACCCTGCTCCAGCAGGCTCTCCGGCTGCCCCC 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 50 BP; 6 A; 18 C; 21 G; 5 T; 0 U; 0 Other;
                                                                                 Turin LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.0%; Scc...
65.9%; Pred. No. o...
... 0; Mismatches
                                                                                 Cantor CR, Andrews BM,
                                                                                                                                                                                                                                                                                         Claim 28; Page 443; 587pp; English
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                         (GENE-) GENELABS TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91US-00723618.
92US-00996783.
93US-00123936.
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(first entry)
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Best Local Similarity 65.93
Matches 29, Conservative
                                                                                                                                                                                                                                 as molecular reagents.
                                                                                                                                         WPI; 1994-234711/28.
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17-SEP-1993;
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17-MAR-1997
                                                                                 Edwards CA,
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AAT64175/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoietin, apposais related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, interferons, interleukins, Grandle colony stimulating factors, complement related proteins cytochromes, kinesins, cytokines, interferons, interleukins, Grandle colony stimulating factors, interferons, interleukins, Grandle colored colo
                                                                                                                                                                                                                                                                                                                                                                                                          Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA protein-binding assay; test sequence; screening sequence; promoter; target; TATA box; Herpes Simplex Virus; HSV_i origin of replication; UD9; transcription factor; TFIID: ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 3.0%; Score 20.2; DB 4; Length 50; Best Local Similarity 88.0%; Pred. No. 7.5e+04; Matches 22; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 50 BP; 6 A; 18 C; 16 G; 10 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 3631; 4143pp; English.
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                                                                                 28-DEC-2000; 2000WO-US035498.
                                                                                                                                         28-DEC-1999; 99US-0173419P.
27-DEC-2000; 2000US-00173419.
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                                                                                                                                                                                                                                                                                      Shimkets RA, Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
                                                                                                                                                                                                                                 (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-465210/50.
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17-SEP-1993;
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03-MAR-1995
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                         05-JUL-2001
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AAQ69713,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequences given in AAFG3713-4312 represent duplex DNA's which act as target regions in the method of the invention. The method for altering the duplex DNA with a small molecule which binds comprises contacting the duplex DNA with a small molecule which binds sequence-specifically to a target region, where, when the small molecule is bound to the target region, it is adjacent to, but not overlapping by more than 4 bp, a binding site for a DNA-binding protein. The small concern the DNA-binding protein, pref. TFIID, to its binding site on the duplex CC the DNA-binding protein to its binding site on the duplex CC of the DNA-binding protein to its binding site on the duplex CC of the DNA-binding protein to its binding site. The compounds isolated using this method are potentially useful as therapeute agents for treatment of any disease which involves a specific DNA sequence, e.g. cancer, or inherited genetic disorders etc. The method is suitable for screening large biological or chemical libraries and allows determination of sequence-specific and relative affinities of known DNA-binding agents for different DNA sequences. The design of these duplex DNA's allows a single DNA:protein interaction to be used for screening sequence. specific, or preferential, DNA binding proteins that recognise almost any possible sequence (see also AAT49539-74). (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                               Altering binding characteristics of DNA binding proteins to duplex DNA - by attaching specific small cpd. to target region close to the protein's binding site, useful in treatment of viral disease, cancer etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Test sequence; DNA-binding molecule; screening sequence; human; nucleic acid amplification; target; viral; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    3.0%; Score 20; DB 2; Length 50;
65.9%; Pred. No. 8.6e+04;
live 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        259 gcgggcacacacacgcgractccaacagggractccggcracccc 302
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Edwards CA
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                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 50 BP; 6 A; 18 C; 21 G; 5 T; 0 U; 0 Other;
Cantor CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cantor CR,
                                                                                                  Claim 6; Col 335-336; 264pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENELABS TECHNOLOGIES INC.
Turin LM, Andrews BM,
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92US-00996783.
93US-00123936.
93US-00171389.
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AAX17463 standard; DNA; 50
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Best Local Similarity 65.9°
Matches 29; Conservative
                        WPI; 1997-020402/02
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                                                                                                                                                                                                                                                                                                                                                                                   correct PF field.)
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17-SEP-1993;
20-DEC-1993;
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Sequences AAX17001 to AAX17600 represent specifically claimed target test
sequences that are used in the method of the invention of determining the
DNA sequence preference of a DNA-binding molecule. The method comprises:

(i) adding a test molecule and a DNA-binding protein to a mixture of
duplex DNA test oligonucleotides, each of the test oligonucleotides
care and a series sequence adjacent to a screening sequence, where the
April of a finity that is independent of the DNA-binding protein with a binding
and where the mixture of duplex DNA test oligonucleotides includes
and where the mixture of duplex DNA test oligonucleotides includes
cand where the mixture of duplex DNA test oligonucleotides includes
several test sequences; (ii) incubating the test molecule, the mixture of
duplex DNA test oligonucleotides and the DNA-binding protein for a time
sufficient to permit binding of the test molecule to test sequences in
the duplex DNA; (iii) separating unbound test oligonucleotides from test
oligonucleotides bound to binding protein; (iv) amplifying the unbound
test oligonucleotides; (v) repeating steps (ii) to (iv); (vi) isolating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the amplified test oligonucleotides; and (vii) sequencing the isolated test oligonucleotides. Test sequences AAX17001-X17481 and AAX17600 correspond to promoter targets for human genes and test sequences AAX17482-X17599 correspond to promoter targets for viral genes
Determination of DNA sequence preference of a DNA-binding molecule -based on inhibition of binding of protein to oligonucleotide sequence attached to test sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 50 BP; 6 A; 18 C; 21 G; 5 T; 0 U; 0 Other;
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                                                                                                                                              Claim 3; Col 337-338; 270pp; English.
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nes 29; Conservative
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WPI; 2002-442819/47.

Decreasing transcriptional activity of genes for treating infections or cancer, by administration of an agent that binds to two non-overlapping regions of the gene.

Example 15; SEQ ID NO 463; 98pp; English.

The invention relates to a method of decreasing transcriptional activity in a duplex deoxyribonucleic acid (DNA) template (T1) comprising contacting (T1) with a binding agent comprising at least one small duplex contacting (T1) with a binding agent comprising at least one small duplex. DNA-binding molecule (T2) coupled to at least one other small duplex. Dinding molecule that binds to a non-overlapping region of target sequence (TS). The method is useful for inhibiting transcription of a range of disease-related genes for treating infections (DY viruses, including human immunodeficiency virus, bacteria, fundi, protozoa and parasites), cancer, cardiovascular, respiratory, gastrointestinal, endocrine/metabolic, rheumatic/immunological, haematological, musculo-section funding in a current disorders. The method provides sequence specific inhibition of transcription of pathological genes without affecting transcription of callular genes regulated by the same transcription factor, and can be applied to regulation of any gene. The method of the invention

Sequence 50 BP; 6 A; 18 C; 21 G; 5 T; 0 U; 0 Other;

0; Gaps Query Match
Best Local Similarity 65.9%; Pred. No. 8.6e+04;
Matches 29; Conservative 0; Mismatches 15; Indels

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Search completed: February 29, 2004, 12:01:06 Job time : 310.274 secs

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Sequence Sequence

Sequence 98, Appl Sequence 25, Appl Sequence 25, Appl Sequence 46, Appl Sequence 2, Appli

nucleic

Run on:

Sequence:

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TITLE OF INVENTION: NOVEL CYCLIN-SELECTIVE UBIQUITIN CARRIER
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CUINTY. WI
COUNTY. WI
COUNTY. United States of America
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: DAYSTEM: PC-DOS/MS-DOS
COFRATING SYSTEM: PC-DOS/MS-DOS
COFRATING SYSTEM: BC-DOS/MS-DOS
COFRATING SYSTEM: BC-DOS/MS-DOS
COFRATE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NOMER: US/10/361,420
FILING DATE: 10-Feb-2003
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/772,156
FILING DATE: 31-Mar-1997
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
; US-10-131-827-25

1 US-09-978-244A-79

1 US-09-978-244A-79

1 US-09-978-255-805-1252

1 US-10-131-877-1253

2 US-10-311-877-253

3 US-10-311-877-2564

4 US-10-076-802-98

5 US-10-076-802-98

1 US-10-33-456-45

5 US-10-33-456-45

6 US-10-35-98-12

1 US-09-778-278-264

1 US-09-778-78-101

1 US-09-78-121

1 US-09-78-121

1 US-09-978-121

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1 US-09-978-133

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1 US-09-978-134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aristarkov, Alexander
Eytan, Esther
Yu, Hongtao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 37, Application US/10361420
Publication No. US20030170866A1
GENERAL INFORMATION:
APPLICANT: Ruderman, Joan V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kirschner, Marc W.
Townsley, Fiona
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hershko, Avram
      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Boston
STATE: MA
      RESULT 1
US-10-361-420-37/c
                     Sequence 37, Appl
Sequence 67, Appl
Sequence 3541, Ap
Sequence 61, Appl
Sequence 5931, Appl
Sequence 67, Appl
Sequence 67, Appl
Sequence 67, Appl
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Sequence 45, Appl
Sequence 6386, Ap
Sequence 6776, Ap
Sequence 57, Appl
Sequence 12, Appl
                                                                                                            February 29, 2004, 11:52:38; Search time 268.199 Seconds (without alignments) 9052.319 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Published Applications NA:*

1. /cgn2_6/ptodata/2/pubpna/PCT_NEW PUB.seq:*
2. /cgn2_6/ptodata/2/pubpna/PCT_NEW PUB.seq:*
3. /cgn2_6/ptodata/2/pubpna/PCT_NEW PUB.seq:*
4. /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
5. /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
6. /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
7. /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
8. /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
9. /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
10. /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
11. /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
12. /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
13. /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
14. /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
15. /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
16. /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
17. /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
18. /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
19. /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
11. /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
11. /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
11. /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
11. /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
11. /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
11. /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
12. /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
13. /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
14. /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
                     GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 US-10-361-420-37

US-09-76-969A-67

US-10-111-827-3541

0 US-09-974-026-61

0 US-09-780-533A-5931

S US-10-131-827-4141

US-09-780-783-436-7723

4 US-10-156-306-7723

4 US-10-156-306-7723

4 US-10-156-366-7723

4 US-10-119-195-45

US-09-740-688A-5776

US-09-740-668A-5776

US-09-740-668A-572
                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                 2353733 seqs, 1803733377 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                         US-09-904-568-3_COPY_294_966
673
                                                                                                                                                                                                                                                                                                                                                                                                                             Listing first 45 summaries
                                                                                  using sw model
                                                                                                                                                                                                                                    IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                nucleic search,
                                    Copyright
                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0 Maximum DB seq length: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Title:
Perfect score:
                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
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Database

NAME: Kerner Ph.D., Ann-Louise

Result

Sequence 2101, Appl Sequence 79, Appl Sequence 12, Appl Sequence 143, Appl

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Gaps

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APPLICANT: Worldemuth, Jay
APPLICANT: Worldemuth, Jay
APPLICANT: Wordward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngcc
ITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNI
ITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
FILE REFERENCE: 50642000120
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR PILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9090
SOFTWARE: PALENTH VOEFSION 3.1
SEQ ID NO 3541
LENGTH: 50
) ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:Exon 11

; OTHER INFORMATION: ('GR2005')

US-09-736-969A-67
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                                                                                                                                                                                        Length 50;
                                                                                                                                                                                                                                                 10; Indels
                                                                                                                                                                                                                                                                                                          510 GCTCCCTGCAGCCGAGCGTCCTGATGCAGCTGAAGC 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 82.1%; Pred. No. 7.4e+04;
Matches 23; Conservative 0; Mismatches 5.
                                                                                                                                                                                 Score 20; DB 9; I
Pred. No. 7.4e+04;
0; Mismatches 10;
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APPLICANT: Davis, Gary
APPLICANT: Delaria, Katherine A
APPLICANT: Christopher, Marlor W
APPLICANT: Christopher, Marlor W
APPLICANT: Daniel, Muller K
TITLE OF INVENTION: Human Bikunin
FILE REPERENCE: 96-223-2Z
CURRENT APPLICATION NUMBER: US/09/974,026
CURRENT FILING DATE: 2001-10-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 09/144,428
PRIOR FILING DATE: 1998-08-31
PRIOR PILING DATE: 1997-03-10
PRIOR FILING DATE: 1997-03-10
PRIOR APPLICATION NUMBER: US 08/725,251
PRIOR PILING DATE: 1996-10-04
PRIOR PILING DATE: 1996-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 439 GGCCTGGCTGCCGCATGTTGCTGACTTT 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 3541, Application US/10131827; Publication No. US20040009479A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 61, Application US/09974026
Publication No. US20030194398A1
                                                                                                                                                                                        Query Match
Best Local Similarity 72.2%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
US-10-131-827-3541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
US-10-131-827-3541
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3.4%; Score 23; DB 14; Length 48;
Best Local Similarity 83.9%; Pred. No. 1.1e+04;
Matches 26; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PATENT NO. US20020068302A1

GENERAL INFORMATION:
APPLICANT: Lu, Peter
APPLICANT: Candia III, Albert Frederick
TILL BEFRENCE: 020054-000411US
CURRENT FILING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: US 60/160,860
PRIOR PILING DATE: 1999-10-21
PRIOR PILING DATE: 1999-10-21
PRIOR PILING DATE: 1999-10-29
PRIOR PILING DATE: 2000-0-114
PRIOR APPLICATION NUMBER: US 60/176,195
PRIOR PILING DATE: 2000-0-1-14
PRIOR APPLICATION NUMBER: US 60/196,267
PRIOR APPLICATION NUMBER: US 60/196,5267
PRIOR APPLICATION NUMBER: US 60/196,527
PRIOR APPLICATION NUMBER: US 60/196,528
PRIOR PILING DATE: 2000-04-11
PRIOR PILING DATE: 2000-04-11
PRIOR PILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: US 60/196,528
PRIOR PILING DATE: 2000-04-11
PRIOR PILING DATE: 2000-04-11
PRIOR PILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: US 60/240,503
PRIOR PILING DATE: 2000-10-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       304 CACCAGCCTGAAGCCTGACACCTTCAGGGAC 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47 caccagecagececeacaceracagerae 17
                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
FRAGMENT TYPE: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-10-361-420-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 67, Application US/09736969A Patent No. US20020068302A1
                                                  REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION
                                                                                                                     (617)526-6000
                                                                                                                                     TELEFAX: (617) 526-5000 INFORMATION FOR SEQ ID NO: 37: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                 LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                     TELEPHONE:
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Gaps
                                                                                                                                                                                                                           Length 50;
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                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 67, Application US/09753436
Patent No. US20110029293A1
GENERAL INFORMATION:
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 120
CORRESPONDENCES ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Boru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Chicago STATE: United States of America CITY: Chicago STATE: United States of America COUNTRY: United States of America COMPUTER: READABLE FORM:
MEDIUM TYPE: Ploppy disk COMPUTER: IBM PC COMPUTER: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/753,436
FILING DATE:
                                                                                                                                                                                                                                                                                                                                   146 AGAAAGTTGCTGAAGTTTGTGGTCAGCAGCCTGC 179
                                                                                                                                                                                                                     Score 19.6; DB 15
Pred. No. 9.5e+04;
0; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                       42 AGAAATTGCTGGGTTTAGCTCTCAGCAGCCGC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
APPLICATION NUMBER: US 08/487,113
FILING DATE: 07-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,754
FILING DATE: 05-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEDLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
RICA PAPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
RICA APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/382,289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Williams, Joseph A., Jr. REGISTRATION VINDER: 38.659
REFERENCE FOOCKET NUMBER: 33282
TELECOMMUNICATION INFORMATION:
  NUMBER OF SEQ ID NOS: 9090
SOFTWARE: Patentin version 3.1
SEQ ID NO 4141
LENGTH: SO
                                                                                                                                                                                                                     Query Match 2.9%;
Best Local Similarity 73.5%;
Matches 25; Conservative
                                                                                                             TYPE: DNA
CORGANISM: Homo sapiens
US-10-131-827-4141
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US-09-753-436-67/c
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Sequence 4141, Application US/10131827

Publication No. US20040009479A1

GENERAL INFORMATION:
APPLICANT: Woldgemuth, Jay
APPLICANT: Woldgemuth, Jay
APPLICANT: Woldgemuth, Jay
APPLICANT: Ly, Ngoc
APPLICANT: Ly, Ngoc
APPLICANT: Ly, Ngoc
TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
FILE REFERENCE: 506612000120
CURRENT APPLICATION WHORER: US/10/131,827
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-10-22
PRIOR FILING DATE: 2001-06-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION; Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-780-533A-5931
                                                                                                                                                                                        ; FEATURE:
; OTHER INFORMATION: Oligonucleotide used in in vitro mutagenesis in Example 9.
US-09-974-026-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ribozymentium:
APPLICANT: Ribozyme arry
APPLICANT: Blatt, Larry
APPLICANT: Chowrira, Bhatt, Jim
APPLICANT: Chowrira, Bhatat
APPLICANT: Chowrira, Botat
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
FILE REFERENCE: MBHBOO, 878-A (400/011)
CURRENT APPLICATION NUMBER: US 60/181,797
FRIOR APPLICATION NUMBER: US 60/181,797
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 6679
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                         Length 45;
                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             311 CTGAAGCCTGACACCTTCAGGGACCAGCTCCAGGAGCTCTGC 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cuegaegaaacucccuucaaegacaucgucceegaecucuec 48
                                                                                                                                                                                                                                                                                                   Score 19.6; DB 10;
Pred. No. 9.4e+04;
0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                              167 GTCAGCAGCCTGCAGGGGAGGACTGCCGAGACG 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36 graceccarcrecaedeccaedreaeceae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5931, Application US/09780533A, Publication No. US20030060611A1 GENERAL INFORMATION:
PRIOR FILING DATE: 1996-03-11
NUMBER OF SEQ ID NOS: 105
SOFTWARE: PatentIn version 3.1
                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 73.5%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-131-827-4141/c
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US-09-780-533A-5931
                                                                                   SEQ ID NO 61
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OTHER INFORMATION: Drimers for ScFv and Fab library generation (Table JOHER INFORMATION: 1) - MHC-Back3
US-09-874-547-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: No. US20020058269Alk, Steffen
APPLICANT: No. US20020058269Alk, Steffen
APPLICANT: Kasner, Paul D.
APPLICANT: Kasner, Paul D.
APPLICANT: Zyomyx, Inc.
TITLE OF INVENTION: Without Clearing of the Cell Culture;
TITLE OF INVENTION: Without Clearing of the Cell Culture;
TITLE OF INVENTION: 2020.44.001110US;
CURRENT APPLICATION NUMBER: US/09/874,547
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/209,503
PRIOR FILING DATE: 2000-06-05
NUMBER OF SEQ ID NOS: 84
SOUTHARR: FastSEQ for Windows Version 3.0
SEQ ID NO SEQ ID NOS: 82
LENGTH: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               271 CACACTGCTCCAGCAGGCCCTCCGTCTGCCCCCCCCACCAGCCTGAA 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45 chgacracracracracracracgacragacraccracagacaca 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.9%; Score 19.4; DB 14;
Best Local Similarity 64.4%; Pred. No. 1.1e+05;
Matches 29; Conservative 0; Mismatches 16;
                                                                                                                                                                                                   APPLICATION NUMBER: US 08/487,113
APPLICATION NUMBER: US 08/487,113
FILING DATE: 07-UN-1995
APPLICATION NUMBER: US 08/286,754
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-UN-1992
APPLICATION NUMBER: US 07/899,724
FILING DATE: 26-MAY-1992
APPLICATION NUMBER: US 07/897,689
FILING DATE: 26-MAY-1992
APPLICATION NUMBER: US 07/827,689
                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/753,436
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-10-163-942-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Williams, Joseph A., Jr.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 33282
                                                                                                                                                                   APPLICATION NUMBER: 09/382,289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/09874547
Patent No. US20020058269A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (312) 474-63 (TELEFAX: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 48 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: singl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
US-09-874-547-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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Sequence 7723. Application US/10156306

Sequence 7723. Application US.0030119017A1

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Levels of IKK-Gamma and PKR
TITLE OF INVENTION: Levels of IKK-Gamma and PKR
TITLE OF INVENTION: Levels of IKK-Gamma and PKR
CURRENT APPLICATION NUMBER: US/10/156,306
CURRENT FILING DATE: 2002-05-28
NUMBER OF SEQ ID NOS: 8013
SOFTWARE: Patentin version 3.0

SEQ ID NO 7723
LENGTH: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-156-306-7723
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| Publication No. US20030199423A1
| GENERAL INFORMATION: US20030199423A1
| GENERAL INFORMATION: US20UX, ROSEMBY
| TITLE OF INVENTION: ICAM-Related Materials and Methods
| UMMBER OF SEQUENCES: 120
| CORRESPONDENCE ADDRESS: 120
| CORRESPONDENCE ADDRESS: 33 South Wacker Drive CITY: Chicago STATE: Illinois COUNTRY: United States of America CONTRY: United States of America COMPUTER READABLE FORM:
| MEDIUM TYPE: Floppy disk COMPUTER: IBM FO. DOS/MS-DOS SOFTWARTE: PATENTIN Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                    Score 19.4; DB 9; Length 48;
Pred. No. 1.1e+05;
0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            271 CACACTGCTCCAGCAGCCCTCCGTCTGCCCCCCCACCAGCCTGAA 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/163,942
FILING DATE: 05-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          324 CCTTCAGGGACCAGCTCCAGGAGCTCTGC 352
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Best Local Similarity 64.4%;
Matches 29; Conservative
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ORGANISM: Artificial Sequence
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 base pairs
                                                                             LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                            TOPOLOGY: linear / MOLECULE TYPE: DNA US-09-753-436-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -10-163-942-67/c
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US-09-740-668A-57/C

is Sequence 57, Application US/09740668A

is TITLE NO. US20020076700A1

is TITLE OF INVENTION: NO. US20020076700A1e1 polypeptides and nucleic acids encoding same price of INVENTION: NO. US20020076700A1e1 polypeptides and nucleic acids encoding same price REPERENCE: 15966-537 CIP

is CURRENT APPLICATION NUMBER: US/09/740,668A

is CURRENT APPLICATION NUMBER: US/09/740,668A

is PRIOR PILING DATE: 1999-12-16

is PRIOR APPLICATION NUMBER: 60/113,485

is PRIOR PILING DATE: 1999-12-16

is PRIOR APPLICATION NUMBER: 60/113,485

is PRIOR PILING DATE: 1999-12-18

is NUMBER OF SEQ ID NOS: 98

is SOFTWARE: Patentin Ver. 2.1

is SEQ ID NOS: 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
2.9%; Score 19.2; DB 15;
Best Local Similarity 87.5%; Pred. No. 1.2e+05;
Matches 21; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.8%; Score 19; DB 9;
81.5%; Pred. No. 1.3e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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               262 AGGCATGCACACTGCTCCAGCA 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262 AGGCATGCACACTGCTCCAGCA 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 AGGAATGCACATTGCTCCAGGA 27
                                                                                                                                                                              Sequence 6776, Application US/10131827
Publication No. US20040009479A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
CRGANISM: Homo sapiens
US-10-131-827-6776
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Best Local Similarity
Matches 22; Conserva
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Publication No. US2004000947941

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Woolgemuch, Jay
APPLICANT: Woolgemuch, Jay
APPLICANT: Woolgemuch, Jay
APPLICANT: Woolgemard, Robert
APPLICANT: Woolgemard, Robert
APPLICANT: Woolgemard, Robert
APPLICANT: Ly, NGWARTON: CHENNIC INFLAMMATORY DISEASES
TITLE OF INVENTION: CHENNIC INFLAMMATORY DISEASES
FILE REFERENCE: 50661200120
CURRENT APPLICATION NUMBER: US 10/006,290
FILE REPEARENCE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-10-22
PRIOR FILING DATE: 2001-10-22
PRIOR FILING DATE: 2001-10-32
SOFTWARE: Patentin Version 3.1
SEQ ID NOS: 9000
SOFTWARE: Patentin Version 3.1
                                                            Gaps
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APPLICANT: ULLMAN, EDMIN
APPLICANT: ULLMAN, EDMIN
APPLICANT: ULLMAN
APPLICANT: ULLMAN
APPLICANT: ULLMAN
TITLE OF INVENTION: ISOTHERMAL AMPLIFICATION IN NUCLEIC ACID ANALYSIS
FILE REFERENCE: 3817.05-1
CURRENT APPLICATION NUMBER: US/10/219,195
CURRENT APPLICATION NUMBER: 00/3-08-14
PRIOR FILING DATE: 2001-08-14
NUMBER: OF SEQ ID NOS: 49
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 45
LENTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: oligonucleotide
(S-10-219-195-45
                                                            ·,
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          Score 19.4; DB 9; Length 50;
Pred. No. 1.1e+05;
0; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             591 TCCAGGAGCTGCGGTACAGCGTGGCCCTGGTCCTAAAGGA 630
                                                                                                     513 CCCTGCAGCCAGCGTCCTGATGCAGCTGAAGCTTTC 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCAAGGAGAAGCTGTGCTACGTCGCCCTGGACTTCGAGCA
                                                                                                                                                     14 cccasccarcarscccassiscascreasics
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Best Local Similarity 87.5%; Pred. No. 1.2e+05;
Matches 21; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                  Sequence 45, Application US/10219195
Publication No. US20030165917A1
GENERAL INFORMATION:
          2.9%;
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                                                            Conservative
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ORGANISM: Homo sapiens
US-10-131-827-6386
Query Match
Best Local Similarity
Matches 26; Conserval
                                                                                                                                                                                                                       RESULT 11
US-10-219-195-45/c
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RESULT 15
US-10-429-849-12/c
| Sequence 1.2 Application US/10429849
| Publication No. US20040029157A1
| GENERAL INFORMATION:
| APPLICANT: TATGARA, MASAAKI
| APPLICANT: TATGARA, MASAAKI
| APPLICANT: TATGARA, MASAAKI
| TILE OF INVENTION: CELL CYCLE-REGULATING PROTEINS
| FILE REPRENCE: 050499/010.
| FILE REPRENCE: 050499/010.
| CURRENT APPLICATION NUMBER: US/09/485,534
| PRIOR APPLICATION NUMBER: US/09/485,534
| PRIOR PILING DATE: 2000-02-14
| PRIOR FILING DATE: 1998-08-17
| PRIOR PILING DATE: 1998-08-17
| PRIOR PILING DATE: 1997-08-15
| NUMBER OF SEQ ID NOS: 19
| SOFFWARE: Patentin Ver. 2.1
| SEQ ID NO 12
| LENGTH: 38
| TYPE: DNA ORANISM: Artificial Sequence: Primer OTHER INFORMATION: Description of Artificial Sequence: US-10-429-849-12
36 AGCGTGGACCTGCTGGAGGAGAAGCTG 10
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Search completed: February 29, 2004, 14:51:52 Job time : 271.199 secs

Query Match 2.8%; Score 19; DB 12; Length 38; Best Local Similarity 71.4%; Pred. No. 1.46+05; Matches 25; Conservative 0; Mismatches 10; Indels

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12, Appl
18, Appl
11, Appl
11, Appl
6, Appl
6, Appl
6, Appl
6, Appl
7358, Appl
7358, Appl
7358, Appl
7358, Appl
7358, Appl
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Sequence 75
Sequence 86
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Sequence 86
Sequence 7,
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APPLICANT: Rischner, Marc W.
APPLICANT: Termsley, Avram
APPLICANT: Townsley, Marc W.
APPLICANT: Townsley, Fiona
APPLICANT: Townsley, Fiona
APPLICANT: Eytan, Esther
APPLICANT: Eytan, Esther
APPLICANT: Yu, Hongrao
TITLE OF INVENTION: NOVEL CYCLIN-SELECTIVE UBIQUITIN CARRIER
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
                                                   Sequence 1
Sequence 1
Sequence 1
Sequence 2
Sequence 5
Sequence 6
Sequence 7
Sequence 6
Sequence 6
Sequence 6
Sequence 7
Sequence 6
Sequence 7
Sequence 6
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,533
FILING DATE: 31-MAR-1997
CLASSIFICATION 1935
ATTORNEY/ASSIFICATION: 435
ATTORNEY/ASSIFICATION: 33,523
REFERENCY DOCKET NUMBER: 33,523
REFERENCY DOCKET NUMBER: 4AZ-015CIP
TELECOMMUNICATION INFORMATION:
TELEFONA: (617) 526-5000
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
INFORMAT
ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: United States of America COUNTRY: United States of America COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
FRAGMENT TYPE: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 37, Application US/08828533 Patent No. 6180379
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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US-08-828-533-37/c
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Sequence 37, Appl
Sequence 5, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 61, Appli
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 67, Appl
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                                                                                                                                                                                                                                                                                         February 29, 2004, 11:48:29; Search time 68.0506 Seconds (without alignments) 5488.301 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 aatgictgctgtgggggctg......gtgagcgcagactgcaggac 673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sued Patents NA:*
/cgn2 6/ptodata/2/ina/5A_COMB.seq:*
/cgn2 6/ptodata/2/ina/5B_COMB.seg:*
/cgn2 6/ptodata/2/ina/6A_COMB.seq:*
/cgn2 6/ptodata/2/ina/6B_COMB.seq:*
/cgn2 6/ptodata/2/ina/PCTUS COMB.seq:*
/cgn2 6/ptodata/2/ina/PCTUS COMB.seq:*
                                                        5.1.6
Compugen Ltd.
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US-09-772-156-37

US-08-772-156-37

US-08-495-6958-5

US-08-495-6958-5

US-09-144-428-61

US-09-144-428-61

US-09-144-428-61

US-08-448-418-10

US-08-448-418-10

US-08-448-418-10

US-08-448-61

US-08-448-67

US-08-487-1130-67

US-08-487-1130-67

US-08-487-1130-67

US-08-487-1130-67

US-08-487-1130-67

US-08-487-1130-67

US-08-487-1105

US-08-114-017-67

US-08-114-017-05

US-08-441-105

US-08-441-105

US-08-441-105

US-08-441-105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               682709 seqs, 277475446 residues
                                                   GenCore version
Copyright (c) 1993 - 2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-904-568-3_COPY_294_966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                    OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0 Maximum DB seq length: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Issued
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Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Title:
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New York
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US-08-176-412-5
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                                                                                                                                                                                                                                                                                         10112
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                                                                                                                                                                                                                                                STATE: Ne
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                                                                                                                                                                                                                                                                                                                                                                                          INVENTION: NOVEL CYCLIN-SELECTIVE UBIQUITIN CARRIER POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/772,156
FILING DATE: 31-Mar-1997
CLASSIFICATION NUMBER: 08/828,533
FILING DATE: 1997-03-31
ATTORNEY/AGENT INFORMATION:
NAME: Kerner Ph. D., Ann-Louise
REGISTRATION NUMBER: 33,523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 3.4%; Score 23; DB 4; Length 48; Best Local Similarity 83.9%; Pred. No. 5.8e+03; Matches 26; Conservative 0; Mismatches 5; Indels
5; Indels
                                      304 CACCAGCCTGAAGCCTGACATTCAGGGAC 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             304 CACCAGCCTGAAGCCTGACACCTTCAGGGAC 334
                                                                             47 caccadecedadecedacetracaderae 17
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 37: US-09-772-156-37
                                                                                                                                                                              Sequence 37, Application US/09772156
Patent No. 6526870N:
GENERAL INFORMATION:
HERSHKO, AVRam
Kirschner, Marc W.
Townsley, Fiona
Aristarkov, Alexander
Eytan, Esther
Yu, Hongtao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: other nucleic acid FRAGMENT TYPE: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (617)526-6000
TELEFAX: (617) 526-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/08176412; Patent No. 5516653; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (617) 526-5, INFORMATION FOR SEQ ID NO: 37; SEQUENCE CHARACTERISTICS;
26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: Un
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: MA
                                                                                                                                            RESULT 2
US-09-772-156-37/c
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US-08-176-412-5/c
Matches
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2.9%; Score 19.8; DB 1; Length 45; 69.2%; Pred. No. 3.3e+04; Live 0; Mismatches 12; Indels
APPLICANT: Bard, Jonathan A.
APPLICANT: Walker, Mary
APPLICANT: Weinshark, Theresa
APPLICANT: Branchek, Theresa
APPLICANT: Beanshank, Richard L.
TITLE OF INVENTION: DNA ENCODING A HUMAN NEUROPEPTIDE
TITLE OF INVENTION: Y/PEPTIDE YY/PANCREATIC POLYPEPTIDE
TITLE OF INVENTION: RECEPTOR (Y4) AND USES THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL NO. 3939/09

APPLICANT: Bard, Jonathan A.

APPLICANT: Walker, Mary

APPLICANT: Walker, Mary

APPLICANT: Walker, Mary

APPLICANT: Weinshauk, Theresa

APPLICANT: Weinshauk, Theresa

TITLE OF INVENTION: DNA ENCOING A HUMAN NEUROPEPTIDE

TITLE OF INVENTION: Y/PEPTIDE YY/PANCREATIC POLYPEPTIDE

TITLE OF INVENTION: RECEPTOR (Y4) AND USES THEREOF

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 GACAGGAGCACGTTCAGAAAGTTGCTGAAGTTTGTGGTC 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 dagagerreacearcagarerregreacearrecreare 6
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
GURRANT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PILING DATE:
CLASSIFICATION: 435
ATONEY/AGANT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 44743/JPW/TEP
TELECOMMUNICATION INFORMATION:
TELEPAN: (212) 977-9550
TELEFAX: (212) 644-022
TELEFAX: (212) 644-022
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERESTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSEE: Cooper & Dunham LLP
F: 1185 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-555-268A-5/c
; Sequence 5, Application US/08555268A
; Patent No. 5958709
                                                                                                                                                                                                                                                      ADDRESSEE: Cooper & Dunham STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 69.2
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                             New York
U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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Gaps
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                                                                                                                                                                                                             12, Indels
                                                                                                                                                                                                                                                     131 GACAGGAGCACGTTCAGAAGTTGCTGAAGTTTGTGGTC 169
                                                                                                                                                                                                                                                                                           44 cagaderreacearcacaarerregicacearceres 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 GACAGGAGCACGTTCAGAAAGTTGCTGAAGTTTGTGGTC
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                                                                                                                                                                     Score 19.8; DB 2;
Pred. No. 3.3e+04;
0; Mismatches 12;
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69.2%; Pred. No. 3.3e+04;
tive 0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION UNDBER: 28,678
REFERENCE/DOCKET UNDBER: 44743-A-PCT\JFW\MAT
TELECOMMUNICATION INFORMATION:
TELEFROM: (212) 278-0400
TELEFRAK: (212) 391-0525
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                  TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYROTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA (genomic)
                                                                                                                                                                       2.9%;
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Best Local Similarity 69.2
Matches 27, Conservative
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Best Local Similarity 69.2
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 45 base pairs
45 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
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STRANDEDNESS: sin
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MOLECULE TYPE: DN
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ANTI-SENSE: NO PCT-US94-14436-5
                                                                                        HYPOTHETICAL: N
HYPOTHETICAL: N
ANTI-SENSE: NO
US-08-495-695B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER:
  LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bard, Jonathan A.
APPLICANT: Bard, Jonathan A.
APPLICANT: Walker, Wheresa
APPLICANT: Walner, Walner, Theresa
APPLICANT: Walner, Theresa
APPLICANT: Walner, Theresa
APPLICANT: Walner, Richard L.
TITLE OF INVENTION: DNA ENCODING A HUMAN NEUROPEPTIDE
TITLE OF INVENTION: Y/PEPTIDE YY/PANCREATIC POLYPEPTIDE
TITLE OF INVENTION: RECEPTOR (Y4) AND USES THEREOF
NUMBER OF SEQUENCES:
ADDRESSED: COOPER & Dunham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC compatible
COMPUTER: ISM PC compatible
COMPUTER: STEMIN PC compatible
COMPUTER: STEMIN PC compatible
COMPUTER: 13-700 brth.
APPLICATION NUMBER: US/08/495,695B
FLING DATE: 13-700-197
CLASSIFICATION 1435
ATTORNEY/AGBNT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/POCKET NUMBER: 44743-A-PCT-US/UPW/JHB
TELECOMMUNICATION INFORMATION:
                                                  CURRAILIUS SISIEM:
CURRAILIUS SISIEM:
CURRAILIUS SISIEM:
CURRAILIUS Patentin Release #1.0, Version #1.25
CURRAILIUS NUMBER: US/08/555,268A

RIING DATE:
CLASSIFICATION NUMBER: US/08/555,268A

FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678

REGISTRATION NUMBER: 28,678

REGISTRATION NUMBER: 28,678

REGISTRATION INFORMATION:
TELEFAME (212) 279-0400

TELEFAME (212) 279-0566

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LEMOTH: 45 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44 cagadetreaceareacaarerregreacarrecreare 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 GACAGGAGCACGTTCAGAAAGTTGCTGAAGTTTGTGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
2.9%; Score 19.8; DB 2;
Best Local Similarity 69.2%; Pred. No. 3.38+04;
Matches 27; Conservative 0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: Cooper & Dunham
1185 Avenue of the Americas
                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08495695B Patent No. 5976814
                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1100
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ANTI-SENSE: NO
US-08-555-268A-5
  MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U
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Gaps
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                                                                          AFFLICANT: Winter, Gregory P
TITLE OF INVENTION: Multivalent and Multispecific Binding
TITLE OF INVENTION: Multivalent and Multispecific Binding
TITLE OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall O'Toole Gerstein Murray and Borun
STREET: 6300 Sears Tower 233 South Wacker Drive
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.9%; Score 19.6; DB 2; Length 46; Best Local Similarity 66.7%; Pred. No. 3.7e+04; Matches 28; Conservative 0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER KEALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
PILING DATE: 14-MAY-1996
CLASSIFICATION: C12N 15/62, 15/70, C07K 1/00
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/02492
PRIOR DATE: 03-DEC-1993
PRIOR DATE: 04-DEC-1992
PRIOR DATE: 04-DEC-1992
PRIOR DATE: 16-JAN-1993
PRIOR DATE: 16-JAN-1993
PRIOR DATE: 10-MAY-1993
PRIOR PRIOR DATE: 10-MAY-1993
PRIOR PRIOR DATE: 10-MAY-1993
PRIOR PREDICATION NUMBER: PC 93303614.7
PRIOR DATE: 10-MAY-1993
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Griffiths, Andrew D
Hoogenboom, Hendricus RJM
Malmqvist, Magnus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: GB 9319969.3
FILING DATE: 22-SEP-1993
ATTONEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-146-979-10
; Sequence 10, Application US/09146979
; Patent No. 6492123
                                                                  McGuinness, Brian T
Pope, Anthony R
Hoogenboom, Hendri
Walmqvist, Magnus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                  arks, James
                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
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APPLICANT: Hollige:
APPLICANT: Griffit!
APPLICANT: Hoogenb.
APPLICANT: Malmqvi
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TOPOLOGY: 15
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                                             APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATEM: PC-DOS/MS-DOS
SOFTWARE: PATEM: Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/144,428
FILING DATE:
                                                                                                                                                                                                                                                                                                                           & Berghoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.9%; Score 19.6; DB 4; Best Local Similarity 73.5%; Pred. No. 3.7e+04; Matches 25; Conservative 0; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 GTCAGCAGCCTGCAGGGGGGACTGCCGAGACG 200
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                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert &
STREET: 300 S. Wacker Drive Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 10-MAR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,106
FILING DATE: 11-MAR-1996
FILING DATE: 11-MAR-1996
FILING DATE: 11-MAR-1996
FILING DATE: 14-JUN 1996
FILING DATE: 14-JUN 1996
FILING DATE: 14-JUN 1996
FILING DATE: 10-MATA
APPLICATION NUMBER: US 08/725,251
FILING DATE: 04-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: CHAO, MATK
REGISTRATION NUMBER: 37,293
REGISTRATION NUMBER: 37,293
REGISTRATION NUMBER: 396,223-II
TELECOMMUNICATION INFORMATION:
TELESCOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/08448418
Patent No. 5837242
GENERAL INFORMATION:
APPLICANT: Holliger, Kaspar-Philipp
                  Sequence 61, Application US/09144428
Patent No. 6583108
GENERAL INFORMATION:
APPLICANT: BAYER CORPORATION, The APPLICANT: DAVIS, Gary
APPLICANT: DAVIS, Gary
APPLICANT: MALLOR, Katherine A APPLICANT: MALLOR, Christopher W APPLICANT: MULLER, Daniel K TITLE OF INVENTION: HUMAN BIXUNIN NUMBER OF SECUENCES: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              not relevant
E: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                     ILLINOIS
                                                                                                                                                                                                                                                                                                                                                                           CITY: CHICAGO
STATE: ILLINOI.
COUNTRY: USA
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MOLECULE TYPE:

US-09-144-428-61
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US-08-448-418-10
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Length 29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Vazeux, Rosemay
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEGURNCES: 116
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borus
STREET: 63100 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CALP: 00600

CAPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: DEM PC Compatible
OPERATING SYSTEM: PC-005/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,882
FILING DATE: 07-JUN-1995
CLASSIFICATION OATA:
APPLICATION NUMBER: US 08/266,754
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATE: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATE: US 08/009,266
FILING DATE: 05-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.9%; Score 19.4; DB 3; 79.3%; Pred. No. 3.7e+04; tive 0; Mismatches 6
CURRENT FILING DATE: 1994-08-11
EARLIER APPLICATION NUMBER: 08/059,189
EARLIER APPLICATION NUMBER: 07/502,559
EARLIER FILING DATE: 1990-03-30
EARLIER FILING DATE: 1990-03-30
EARLIER FILING DATE: 1980-06-24
EARLIER FILING DATE: 1980-06-24
EARLIER FILING DATE: 1987-06-24
NUMBER OF SEQ ID NOS: 84
SOFTWARE: PARISEQ for Windows Version 3.0
SSC ID NO 45
LENGTH: 29
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FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5773218and, Greta E.
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 67, Application US/08482882
Patent No. 5773218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
CORGANISM: Homo sapiens
US-08-297-395-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Chicago STATE: Illinois COUNTRY: Irc.
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                                                             APPLICANT: Winter, Gregory P. TITLE OF INVESTION: Multivalent and Multispecific Binding TITLE OF INVESTION: Multivalent and Multispecific Binding NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall O'Toole Gerstein Murray and Borun STREET: 6300 Sears Tower 233 South Wacker Drive CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
2.9%; Score 19.6; DB 4; Length 46;
Best Local Similarity 66.7%; Pred. No. 3.7e+04;
Matches 28; Conservative 0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/146,979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     510 GCTCCCTGCAGCCAGCGTCCTGATGCAGCTGAAGCTTTCAG 551
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Patent No. 6039947
Batent No. 6039947
APPLICANT: Howard L. Weiner
APPLICANT: David A. Hafler
APPLICANT: David A. Hafler
APPLICANT: David A. Pafler
APPLICANT: David A. Pafle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 geggéceageceargaceceageraceageraaagaagreaa 45
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/448,418
FILING DATE: 14-MAY-1996
APPLICATION NUMBER: PCT/GB93/02492
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9225453.1
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: EP 93303614.7
FILING DATE: 10-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9319969.3
FILING DATE: 22-SEP-1993
ATTORNEY-AGENT INFORMATION:
NAME: DAVIG W. Clough
REGISTRATION NUMBER: 36,107
REFERENCEY-DOKKET NUMBER: 28111/3265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28111/32651
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, MOLECULE TYPE: DNA primer
US-09-146-979-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
US-08-297-395-45/c
                                                APPLICANT:
APPLICANT:
APPLICANT:
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Length 48;
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                                                                                                                                                                                                                         Query Match 2.9%; Score 19.4; DB 1; Length 4 Best Local Similarity 64.4%; Pred. No. 4.2e+04; Matches 29; Conservative 0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               45 chahcrachachachcchcachcanchachchachachachachachacha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazewi, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTACKED TO THE STATE OF THE ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08 6,754
FILING DATE: 05-AUG-1994
PRIOR APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-APA-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 26-AUX-1992
PRIOR APPLICATION NUMBER: US 07/899,724
FILING DATE: 26-MAX-1992
PRIOR APPLICATION NUMBER: US 07/827,689
FILING DATE: 26-MAX-1992
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-ANA-1992
ATCANEY/AGENT INFORMATION:
NAME: NO. SB37822And, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 37744
TELECHOME: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
1S-08-487-113D-67/c
Sequence 67, Application US/08487113D
Patent No. 5837822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
WOLECULE TYPE: DNA
US-08-483-389-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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CORRESPONDENCE ADDRESSE

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 233 South Wacker Drive/6300 Sears Tower CITY: Chicago
STRATE: 1linois

COUNTRY: United States of America

ZIP: 6066

COMPUTER READABLE FORM:
MUDIUM TYPE: Floppy disk
COMPUTER: BAR PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ParentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,389

FILING DATE: 07-UN-1995

CLASSIFICATION NUMBER: US 08/102,852

FILING DATE: 05-AUG-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061

FILING DATE: 2-JAN-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724

FILING DATE: 2-JAN-1992

PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724

FILING DATE: 2-JAN-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724

FILING DATE: 2-JAN-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724

FILING DATE: 2-JAN-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724

FILING DATE: 2-JAN-1992

ATTORNEY/AGBNT INFORMATION:
NAME: SUM, YOUNG 7.
DATA 337

DATTORNEY/AGBNT INFORMATION:
NAME: SUM, YOUNG 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 2.9%; Score 19.4; DB 1; Length 48; Best Local Similarity 64.4%; Pred. No. 4.2e+04; Matches 29; Conservative 0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                271 CACACTGCTCCAGCAGGCCCTCCGTCTGCCCCCCCCACCAGCCTGAA 315
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APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-RELATED PROTEIN
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSEE: MATSHALI, O'Toole, Gerstein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Suh, Young J.
REGISTRATION NUMBER: P-41,337
REFERENCE/DOCKET NUMBER: 27866/32760
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 67, Application US/08483389 Patent No. 5811517
                                    TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-6448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NE: (312) 474-6300
: (312) 474-0448
(312) 474-6600
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                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-482-882-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
US-08-483-389-67/C
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                                271 CACACTGCTCCAGCAGGCCCTCCGTCTGCCCCCCCCACCAGCCTGAA 315
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                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: 11linois
COUWRY: USA
ZIP: 60606
                                                                                    45 CAGACTGCTGCAGTTGCACCTCGGACTGGACACCCTGCGGCGCCGCAA 1
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Flam PC Compatible
COMPUTER: Flam PC Compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,932
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: 08/286,754
FILING DATE: 05-AUG-1994
FILING DATE: 05-AUG-1994
FILING DATE: 05-AUG-1993
FILING APPLICATION NUMBER: US 08/102,865
FILING DATE: 22-JAN-1993
PRIOR APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION NUMBER: US 07/894,061
FILING DATE: 26-MAY-1992
PRIOR APPLICATION NUMBER: US 07/894,061
FILING DATE: 27-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/897,689
FILING DATE: 27-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/887,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                       Sequence 67, Application US/08483932
Patent No. 5880268
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: NO. 5880268and, Greta E. REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32178
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TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                     RESULT 15
US-08-483-932-67/c
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2.9%; Score 19.4; DB 2; Length 48;
Best Local Similarity 64.4%; Pred. No. 4.2e+04;
Matches 29; Conservative 0; Mismatches 16; Indels
                                                              Query Match 2.9%; Score 19.4; DB 2; Length 48; Best Local Similarity 64.4%; Pred. No. 4.2e+04; Matches 29; Conservative 0; Mismatches 16; Indels
                                                                                                                                                                                                     271 CACACTGCTCCAGCAGCCCTCCGTCTGCCCCCCCCACCAGCCTGAA 315
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 57, Application US/08473503
Patent No. 5869262
GENERAL INFORMATION:
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                       45 chgacriccriccaccricgacricgacricgacrecgeccan 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
APPLICATION NUMBER: US/08/473,503
FILING DATE: 05-AUG-1994
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
RIOR APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
RIOR APPLICATION NUMBER: US 07/894,061
FILING DATE: 22-JAN-1992
RIOR APPLICATION NUMBER: US 07/894,061
FILING DATE: 25-JAN-1992
RIOR APPLICATION NUMBER: US 07/894,061
FILING DATE: 27-JAN-1992
APPLICATION NUMBER: 35,302
REGISTRATION FOR SEQ ID NO: 67: SEQUENCE CHARACTERISTICS:
LEBNGTH: 48 base pairs
TURNED THE ABB TO THE ABB TELEX: CLEAR TELEX: CLEAR
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nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 6300 Sear
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: DNA US-08-473-503-67
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US-08-473-503-67/c
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US-08-487-113D-67
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Gaps

Search completed: February 29, 2004, 14:42:41 Job time: 70.0506 secs

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Run on:

Sequence: Title: Perfect

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AII53463 uc53e11.r
AU102937 AU102937
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AU103175 AU1020175
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AU103175 AU1020175
BIE 60469 602864532
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CG708675 1119010CC
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CG70884 1119011CC
CG70889 1119011CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUI02670 50 bp mRNA linear EST 30-AUG-2001 AUI02670 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone CAS07213, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryotta.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 50)

Suzuki,Y., Taira,H., Teunoda,T., Mizushima-Sugano,J., Sese,J.,

Hata,H., Ora,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,

Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.

Diverse transcriptional initiation revealed by fine, large-scale

mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Email: Shirokanedal Minatoku, Tokyo 108-8639, Japan
Email: yenzukidims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                          B1160469
CG714548
CG708599
CG708605
                                                                                                                      CG708624
CG708627
CG708670
CG708679
CG708716
CG708716
CG708750
CG708750
CG708750
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CG708616
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AU102670.1 GI:13552191
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AU102670/c
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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MEDLINE
PUBMED
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
AL946896 Arabidops
BG772081 602721525
H45385 yn99c12.rl
                                                                 2004, 10:34:43; Search time 2034.51 Seconds (without alignments) 9878.168 Million cell updates/sec
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                                                                                                                            aatgtotgctgtgggggctg.....gtgagcgcagactgcaggac 673
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                                                                                                                                                                                                    138346
       GenCore version 5.1,6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                              27513289 segs, 14931090276 residues
                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                      US-09-904-568-3_COPY_294_966
673
1 aatgtctgctgtgggggctg......
                                             nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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AL946896
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Gapop 10.0 , Gapext 1.0
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em_gss_phg: *
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gb_gssl: *
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em_estinm:*
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em_estil:*
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gb_esti:*
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mus:*
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                 Copyright
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Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3333
                                                                                                                     score:
                                                                                                                                                Scoring table:
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20.8
20.6
20.6
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Database :

Result No.

0 0 0 0

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/lab_host="ITMAGE:483827"
/lab_host="ITMAGE:483827"
/clone=lib="NIH MGC 97"
/clone=lorgan: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (Grega); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTVV-3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BG772081 45 bp mRNA linear EST 15-MAY-2001
602721525F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4838287 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST 31-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 45)
processed for submission. T-DNA derived sequences were removed."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: Gapabs-remail.nih.gov

Tissue Procurement: Wiklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shira

Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                       Gaps
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http://image.llnl.gov
Plate: LLAM1072 row: a column: 08
High quality sequence stop: 45.
Location/Qualifiers
                                                                                                                                                                                                                                                              634
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                                                                                                                                                                                                                                                                                                                         41 GGATCTGCTTTTTCTGCGTGGCCTTTGTGGTAATGGACAAG
                                                                                                                                                                                                                                                              595 GGAGCTGCGGTACAGCGTGGCCCTGGTCCTAAAGGAGGATG
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llarity 67.4%; Pred. No. 1.7e+06;
Conservative 0; Mismatches 14;
                                                                                                                                     Score 20.8; DB 29;
Pred. No. 1.6e+06;
0; Mismatches 12;
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/db_xref="taxon:9606"
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                                                                                                                                         3.1%;
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                                                                                                                                  Query Match
Best Local Similarity 70.03
Matches 28; Conservative
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BG772081
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Matches 29; Conserv
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BG772081/c
LOCUS
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ORGANISM
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H45385/c
LOCUS
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             Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
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(flanking sequence tags) from Arabidopsis thaliana T-DNA
transformed lines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         269 CACACACTGCTCCAGCAGGCCCTCCGTCTGCCCCCCACCAGCCTGAAGC 317
                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/db_cxrefA="taxon:9606"
/clone="lib="Sugano Homo sapiens CDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 3.2%; Score 21.8; DB 9; Length 50; Best Local Similarity 65.3%; Pred. No. 1e+06; Matches 32; Conservative 0; Mismatches 17; Indels
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/mol_type="genomic DNA"
/strain="Columbia 0"
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                                                                    149-156 (1997).
Location/Qualifiers
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EST 17-FEB-1995

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yc23e03.rl Stratagene lung (#997210) Homo sapiens CDNA clone
IMAGE:81532 5' similar to gb:X55715 408 RIBOSOMAL PROTEIN S3
(HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
Insert Size: 55
                                                                                                                                                                                                                                                                  Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="male"
                                                                                                                                                                                T63738.1 GI:667603
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VERSION
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         RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1952)
Contact: Wilson RK
Washington University School of Medicine
A444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Fax
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                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (Dases 1 to 46)
Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Parsons,J., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Pohlfing,T., Soares,M., Tan,F., Treyaskis,E., Waterston,R., Williamson,A., Wohldman,P. and
yn99c12.rl Soares adult brain N2b5HB55Y Homo sapiens cDNA clone
IMAGE:176566 5' similar to SP:TFS2_MOUSE P10712 TRANSCRIPTION
FACTOR S-II ;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   351 GCATCCCCCAAGACCTGGTCGGGGACTTGGCCAGCG 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="GDB:3838762"
/db_xref="taxon:9606"
/clone="IMAGE:176566"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: M13RP1
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                            The WashU-Merck EST Project
                                                                                                                                                                          Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="Male"
                                                                                                                H45385.1 GI:921437
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nes 26; Conservative
                                                                                                                                                                                                         Homo sapiens
                                                                                        H45385
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   DEFINITION
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Matches
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High qality sequence stops: 37 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 55 Std Error: 0.00
Seq primer: M13RP1
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hulfman, M., Kucaba, T., Lacy, M., Le, M., Le, M., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohliing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                                                                                    Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AII53463 46 bp mRNA linear EST 30-SEP-uc53e11.rl Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:1429388 5' similar to SW:PHLX_RABIT Q05017 PHOSPHOLIPASE
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                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.9%; Score 19.8; DB 14; Length 45; 77.4%; Pred. No. 2.5e+06;
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AI153463
AI153463.1 GI:3681932
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/organism="Homo sapiens"
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/db_xref="GDB:485149"
/db_xref="taxon:9606"
/clone="IMAGE:81532"
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Location/Qualifiers
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VERSION
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Contact: Yutaka Suzuki
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirorkanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-chyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a S'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
                                                                                                                                                                                                           Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Ysbaltcomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AU103175 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone AU1057628, mRNA sequence.
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1 (bases 1 to 50)

2 (bases 1 to 50)

3 (bases 1 to 50)

4 (bases 1 to 50)

Butuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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/clone="LM010694"
/clone_lib="Sugano Homo sapiens cDNA library"
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Pred. No. 2.7e+06;
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2.9%; Score 19.8; D:
Best Local Similarity 69.2%; Pred. No. 2.7e
Matches 27; Conservative 0; Mismatches
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/organism="Homo sapiens"
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Location/Qualifiers
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                                                                                                                                                                                     Contact: Yutaka Suzuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
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AU103175/c
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KEYWORDS
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                                                  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1 (Dases 1 to 46)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenerg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 50)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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0
                                                                                                                                                                                                                                                                                                       Contact: Marra M/Mouse EST Project
WashU-HMMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.9%; Score 19.8; DB 9;
ilarity 69.2%; Pred. No. 2.6e+06;
Conservative 0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Mus musculus"
                                                                                                                                                                                                                                      Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1429388"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tissue_type="Thymus"
dev_stage="4 weeks"
lab_host="DH103"
                                    Mus musculus (house mouse)
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Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sex="male"
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Matches 27; (
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                                                                                                                                                   AUTHORS
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              KEYWORDS
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Sanger Xenopus tropicalis EST project 2001 (11_2003)
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/db_xref="taxon:9606"
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BI160469.1 GI:14620470
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                                     Contact: Huckle E
                                                       Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence.
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BI160469/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ina.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
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ARAL Sequence.
AL651763
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Silurana tropicalis
Sukaryota, Metazoa; Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia; Batrachia, Anura, Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                        AU106019

AU106019 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone (XAIA1053, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                             Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S. Dipierse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (S), 388-393 (2001)
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1 (bases 1 to 50)
Croning, M. D. R., Ashurst, J. L., Taylor, R., Zorn, A. M. and Rogers, J.
                                                       Gaps
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/clone_lib="Sugano Homo sapiens cDNA library"
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                                                                                             268 GCACACACTGCTCCAGCAGGCCCTCCGTCTGCCCCCCCCACCAGCCTGA 314
                   Length 50;
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               Score 19.8; DB 9;
Pred. No. 2.7e+06;
0; Mismatches 17;
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63.8%; Pred. No. 2.7e+06;
tive 0; Mismatches 17;
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                 ch 2.9%;
1 Similarity 63.8%;
30; Conservative
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Email: trop@sanger.ac.uk
This sequence is from a Xenopus Gene Collection (XGC) library
Constructed by Aaron M. Zorn.
Constructed by Aaron M. Zorn.
Gonstructed by Aaron M. Zorn.
Sorn.
Sastrulae. BCORI-NotI cut CDNA was then ligated into pCS107 with
BCORI at the 5' end and NotI at the 3' end.
Vector: pCS107, Site 1: BCORI; Site 2: NotI
Host: Bscherichia coli XL1_blue
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/lab_host="Escherichia coli XL1-blue" |
/clone lib="XGG-gastrula" |
/note="Vector: pCS107; Site 1: EcoR1; Site 2: NotI; cDNA was oligo dT primed from Sug of poly A+ RNA from stages 10-13 gastrulae: EcoR1-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."
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602864532F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:5018743 5',
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TROPICALIS SEQUENCE ID: TGas036n06.plkSP6
Sequencing-primer: SP6.
Location/Qualifiers
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Pred. No. 2.9e+06;
0; Mismatches 19;
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/clone="TGas036n06"
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plates with ampicillin."

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CG708599 44 bp DNA linear GSS 20-OCT-2003
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stanford University
855 California Ave, Palo Alto, CA 94304, USA
8221
8231: Walbot@stanford.edu
8247 probable ligation site of ends cut by single endonuclease.
82484786 complemented post-ligation sequence from source sequence.
Plate: 1119010 row: 33
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/cultivar="mixed background W23/A188/B73/X55"
/db_xref="taxon:4577"
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                                                                                Length 43;
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                                                                                                                                                                          229 CCTGCCGGAGGAGCAGCTGGGTGCCCTGCTGGCAGGCATG
                                                                           Score 19.2; DB 29;
Pred. No. 3.3e+06;
0; Mismatches 13;
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ilarity 67.5%; Pred. No. 3.3e+06;
Conservative 0; Mismatches 13;
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/organism="Zea mays"
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Location/Qualifiers
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                                                                             Query Match 2.9%;
Best Local Similarity 67.5%;
Matches 27; Conservative (
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/clone="IMAGE:5018743"
/tissue type="spithalioid carcinoma cell line"
/lab host="bhi08 (phage-resistant)"
/clone_lib="NIH MGC_42" resistant)"
/clone_lib="NIH MGC_42" vestistant)"
/clone_lib="NIH MGC_42" vestistant)"
/note="Grgan: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: ECORI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5 adaptor: aGGAGGGGG(G). Size-selected >SOUDP
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
Callifornia, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |
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// (Colliva="mixed background W23/A188/B73/K55"
// (Colliva="mixed background W23/A188/B73/K55"
// (Lissue type="leaf"
// (Lissue type="leaf"
// (Lissue type="leaf"
// (Lone lib="lill9" RescueMu Grid AA"
// (Lone lib="lill9" RescueMu Grid and Lib BamHi; Site 2: BglII;
// (Lone lib="lill9" RescueMu Grid genomic DNA.
// (RescueMu is a 4.9 kb modified maize Mu transposon
// (RescueMu is a 4.9 kb modified maize Mu transposon
// (RescueMu is a 4.9 kb modified maize Mu transposon
// (RescueMu is a 4.9 kb modified maice from total genomic DNA.
// (RescueMu is a 4.9 kb modified maice modicion
// (RescueMu is Grid AA was grown at UC San Diego in 2002. DNA
was extracted from leaf strips, double digested using
// (BamHi and BglII, and ligated to form circular plasmids.
// (BH10B cells were transformed and then screened on LB
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Stanford University
Stanford University
BES California Ave, Palo Alto, CA 94304, USA
BES California Ave, Palo Alto, CA 94304, USA
Fax: 650 723 2227
Fax: 650 725 821
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Very probable ligation site of ends cut by single endonuclease.
Plate: 1119037 row: 32
Class: transposon-tagged.
Class: transposon-tagged.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     346 GCTCTGCATCCCCCAAGACCTGGTCGGGGACTTGGCC 382
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/clone_10b=_1119 - RescueMu Grid AA"
/clone_10b=_1119 - RescueMu Grid AA"
/clone_10red A.9 kb, modified : BamHI; Site_2: BgllI;
RescueMu is a 4.9 kb, modified maize Mu transposon
Gesigned to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.rambbi.iastate.edu' and follow the links for
'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA
was extracted from leaf strips, double digested using
BanHI and BglII, and ligated to form circular plasmids.
DHIOB cells were transformed and then screened on LB
plates with ampicillin."
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Contact: Walbot V
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
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/ta; Liliopsida; Poales; Poaceae; PACCAD
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Stanford University
Stanford University
Tel: 650 723 2227
Fax: 650 725 8221
Fax: 610 725 8221
Fax: 620 7
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CG708605
CG708605.1 GI:37734511
GSS.
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/clone_lib=_Ill9 - RescueMu Grid AA"
/clone_lib=_Ill9 - RescueMu Grid AA"
/note=_Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamH1; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Wu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site, www.radbiastate.edu' and follow the links for KescueMu. Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using .BamH1 and BglIII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin.
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                                                                                              Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001) Contact: Malbot V
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                                                                                                                                                                                                                                           Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 550 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
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clade; Panicoideae; Andropogoneae; Zea.
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Job time : 2037,51 secs
                                                                                                                                                                                                             Department of Biological Sciences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Class: transposon-tagged.
Location/Qualifiers
                                     (bases 1 to 44)
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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February 29, 2004, 10:05:33 ; Search time 2729.03 Seconds (without alignments) 10688.739 Million cell updates/sec US-09-904-568-3_COPY_294_966 673 1 aatgtctgctgtggggggttg.....gtgagcgcagactgcaggac 673 3470272 seqs, 21671516995 residues OM nucleic - nucleic search, using sw model IDENTITY NUC Gapop 10.0 , Gapext 1.0 Title: Perfect score: Sequence: Scoring table: Searched: Run on:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 50

Total number of hits satisfying chosen parameters:

1603530

GenEmbl:* Database :

gb_htg:.*
gb_oom:.*
gb_oom:.*
gb_bht:.*
gb_bht:.*

em_htg_vrt:*

is the number of results predicted by chance to have a Pred. No.

em_htgo_mus:* em_htgo_other:* htgo hum: *

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

source

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FEATURES

KEYWORDS SOURCE ORGANISM

source

ORIGIN

TITLE JOURNAL FEATURES

REFERENCE AUTHORS

RESULT 2 AR285578/c LOCUS

DEFINITION

ACCESSION VERSION

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalià; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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45 CTGCTGATCTACAGAGTTTCCAACCGATTTTCTGGTGTGCCAAGG 1
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Detection of genetic polymorphisms
Patent: WO 02052044-A 5840 04-JUL-2002;
Riken (JP)
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3.1%; Score 20.6; DB 6;
Best Local Similarity 74.3%; Pred. No. 7.6e+06;
Matches 26; Conservative 0; Mismatches 9;
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3.1%; Score 20.6; DB 6;
Best Local Similarity 74.3%; Pred. No. 7.6e+06;
Matches 26; Conservative 0; Mismatches 9;
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Sequence 3311 from Patent WO02052044.
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AX517113/c
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E41550/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unidentified
unidentified
unclassified.
1 (bases to 45)
Taylor, G. and Stott, E.J.
ANTIBODIES FOR TREATMENT AND PREVENTION OF RESPIRATORY SYNCYTIAL
VIRUS INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Ruderman, J.V., Hershko, A., Kirschner, M.W., Townsley, F.,
Aristarkov, A., Sytan, E. and Yu, H.
Cyclin-selective ubiquitin carrier polypeptides
Patent: US 6528633-A 37 04-MAR-2003;
Location/Qualifiers
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                                                                                                                       Length 48;
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3.4%; Score 23; DB 6; Length 48;
Best Local Similarity 83.9%; Pred. No. 2.5e+06;
Matches 26; Conservative 0; Mismatches 5; Indels
                                                                                                                                                          5; Indels
                                                                                                                   Query Match
3.4%; Score 23; DB 6; I
Best Local Similarity 83.9%; Pred. No. 2.5e+06;
Matches 26; Conservative 0; Mismatches 5;
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SCOTGEN LTD (GB); TAYLOR GERALDINE (GB)
Location/Qualifiers
                                                                                                                                                                                                304 CACCAGCCTGAAGCCTGACACCTTCAGGGAC 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             304 CACCAGCCTGAAGCCTGACACCTTCAGGGAC 334
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/mol_type="unassigned DNA"
/db xref="taxon:32644"
                         1. .48
/organism="unknown"
/wol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="unknown".
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                Sequence 37 from patent US 6528633.
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Sequence 40 from Patent WO9320210.
A76101
A76101.1 GI:6088242
    Location/Qualifiers
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DEFINITION ACCESSION VERSION KEYWORDS

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RESULT 3

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                                                                                                                                              Gallus gallus gallus Mutazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Aves, Neognathae, Galliformes, Phasianinae, Gallus.

1 (bases 1 to 50)

Kume,A., Koyata,H., Sakakibara,T., Ishiguro,Y., Kure,S. and Hiraga,K.
                                                                                                                                                                                                                                                                                                                                                           These data kindly submitted in computer readable form by: Koichi
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                                            החאטטטט
Gallus gallus gene for glycine decarboxylase, partial cds.
D90240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Gallus gallus"
/mol_type="ganomic DNA"
/db xref="taxon:9031"
/note="glones pCP[15b, 23a, 110b, and 112a]"
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3.0%; Score 20; DB 5; Length 50;
Best Local Similarity 65.9%; Pred. No. 9.5e+06;
Matches 29; Conservative 0; Mismatches 15; Indels
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//note="pyridoxal phosphate enzyme"/
/codon_start=1
/product="glycine decarboxylase"/
/proctein_id="BAAL427.1"/
/db_xref="Gl:222819"/
/translation="MOSCGRWWGRLAA"
                                                                                                                                                                                                                                                                                                                                                                                                    Toyama Medical and Pharmaceutical University School of Medicine
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Clasp-4 transmembrane procesin
Patent: WO 0142294. 67 14-JUN-2001,
Arbor Vita Corporation (US)
Location/Qualifiers
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Sequence 67 from Patent W00142294.
AX173088.1 GI:14597988
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81-764-34-4656.
Location/Qualifiers
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synthetic construct
artificial sequences.
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AX173088/c
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                  RESULT 8
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KAZUYUKI HAMADA, FUMIO NAKAKIDO
A01H5/00, C12N5/10, C12N15/09, C12N5/00, C12N15/00 CC
                                                                                                                                                                                                                                                                                                                                                                                                        3.0%; Score 20.2; DB 6; Length 42; 68.3%; Pred. No. 9e+06; tive 0; Mismatches 13; Indels
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synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 42)
Hamada,K. and Nakakido,F.
Method for producing male sterile plant
Patent: WO 0124616-A 2 12-APR-2001;
JAPAN TOBACCO INC, KAZUYUKI HAMADA, FUMIO NAKAKIDO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       482 GTAGCAATCTCCACCAGTGCCCTGGCTCGCTGCAGCC 522
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                           synthetic construct
artificial sequences
artificial sequences.
1 (bases 1 to 42)
Hamada,K. and Nakakido,F.
Method for yielding male abortive plants
Patent: JP 2001095406-A 2 10-APR-2001;
JAPAN TOBACCO INC
PN JP 2001095406-A/2
PD 10-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-5EP-2000 WO 2000JP006222
30-5EP-1999 JP 99P 279307
KAZUYUKI HAWADA, PUMIO NAKAKIDO
A01H5/00, CIZNI5/11, CIZNI5/63, CIZNI5/82
Primer 172del-R
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    .42
    ^2organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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BD013091
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WO 0124616-A/2
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Best Local Similarity 68.3
Matches 28; Conservative
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28; Conserval
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PD 10-A1
PF 30-S1
PI KAZU
PC A01H:
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Matches 28
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BD013091/c
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Location/Qualifiers
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JP 2002522029-A/169.
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                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 45)
Bard,J.A., Walker,M.W., Branchek,T. and Weinshank,R.L.
Processes for identifying compounds that bind to the human Y4
                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 45)
Bard, J.A., Walker, M.W., Branchek, T. and Weinshank, R.L.
DNA encoding a human neuropeptide Y/peptide Y/pancreatic
polypeptide receptor (Y4) and uses thereof
Patent: US 5976814-A S 02-NOV-1999;
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2.9%; Score 19.8; DB 6; Length 4
Best Local Similarity 69.2%; Pred. No. 1.1e+07;
Matches 27; Conservative 0; Mismatches 12; Indels
                                                                                        Length 50;
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/mol_type="taxon:32630"
/noFe="Exon II ('GR2005')"
                                                                                     3.0%; Score 20; DB 6; I
Local Similarity 72.2%; Pred. No. 9.5e+06;
Les 26; Conservative 0; Mismatches 10,
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/organism="unknown"
/mol_type="unassigned DNA"
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/wol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent: US 5958709-A 5 28-SEP-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45 bp
Sequence 5 from patent US 5976814.
AR083198.1 GI:10009988
                                                                                                                                                                                                                                                    AR075912 45 bp
Sequence 5 from patent US 5958709.
AR075912
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                                                                                                                                                                                                                                                                                                                                            Unknown.
Unclassified.
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AR075912/c
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AR083198/c
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FEATURES
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synthetic construct

synthetic construct

artificial sequences.

I (bases 1 to 45)
Sidhu,S.S., Weiss,G.A. and Wells,J.A.

Improved transformation efficiency in phage presentation by modification of coat proteins

Datent: JP 2002522029-A 169 23-JUL-2002;

Canenymeth INT Sequence

NO Artificial Sequence

NO Artificial Sequence

PP 23-JUL-1999 JP 2000562499

PP 22-JUL-1999 US 60/094291,08-OCT-1998 US 60/103514 PR 27-JUL-1999 US 60/133296,19-MAY-1999 US 60/133296,19-MAY-
BD247107 45 bp DNA linear PAT 17-JUL-2003 Improved transformation efficiency in phage presentation by modification of coat proteins.
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Bard, J.A., Walker, M.W., Branchek, T. and Weinshank, R.L.
DNA encoding a human neuropeptide Y/peptide Y/pancreatic
polypeptide receptor (Y4) and uses thereof
Patent: US 5516653-A 5 14-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö

    .45
    organism='Artificial Sequence'

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2.9%; Score 19.8; DB 6;
Best Local Similarity 69.2%; Pred. No. 1.1e+07;
Matches 27; Conservative 0; Mismatches 12;
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/organism="synthetic construct"
/mol_type="genomic DNA"
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 5 from patent US 5516653.
I20781.
I20781.1 GI:1601136
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Search completed: February 29, 2004, 13:32:19
Job time : 2734.03 secs
                                  SUSSEEE
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23-DEC-1999 JP 2000591219
23-DEC-1998 GB 9828256.9
RAKESH ANAND, JOHN EDWARD NORRIS MORTEN, JOHN CRAIG SMITH PC
5/09, AGIN31/711, AGIK48/00, AGIP3/04, AGIP3/10, AGIP7/00, PC
                                                                                                                                                                                                                                                          artificial sequences.

1 (bases 1 to 48)
Anado,R., Morten,J.E.N. and Smith,J.C.
Anado,R., Morten,J.E.N. and Smith,J.C.
Anado enclocited polymorphism of human pyruvate dehydrogenase
kinase isoenzyme 2 (PDK2)
Patent: JP 2002533135-A 8 08-OCT-2002;
    Gaps
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ASTRAZENECA AB, THE VICTORIA UNIVERSITY OF MANCHESTER
APPLICATE Sequence
BN JP 2002542830-A/8
PP 17-DEC-2002
PP 28-APR-2000 JP 2000615774
PR 01-MAY-1999 GB 9910077.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 48;
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Pred. No. 1e+07;
0; Mismatches 17; Indels
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description of Artificial Sequence: Primer
                              131 GACAGGAGCACGTTCAGAAGTTGCTGAAGTTTGTGGTC 169
                                                            44 GAGAGGITCACGATCAGAATGITGGIGACATICCICATC 6
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synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 48)
Castro,M.G., Emery,S.C. and Lowenstein,P.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers

    .48
    ^4sganism="synthetic construct"
|mol_type="genomic DNA"
|db_xref="taxon:32630"

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   Mismatches
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JP 2002533135-A/8
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Best Local Similarity 63.8%;
Matches 30; Conservative
                                                                                                                                                                                                                                synthetic construct
synthetic construct
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 Conservative
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27;
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BD270516/c
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BD237452/c
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TITLE
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C12N15/09, A61K31/198, A61K31/222, A61K35/76, A61K38/00, A61K38/44,
                                                               AGIK38/46,
AGIK48/00,AGIP35/00,AG1P43/00,C12N15/00,AG1K37/54,AG1K37/02,
MARIA GRACIELA CASTRO, STEPHEN CHARLES EMERY, PEDRO RICARDO
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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    .48
/organism='Artificial Sequence'

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Description of Artificial Sequence: Primer
Kev
                                                                                                                                                                                                                                            1. .48
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Sequence 5574, A equence 5, Appli

Sequence Sequence 28 Sequence 28 Sequence 28 Sequence 28 Sequence 28 Sequence 28 Sequence 28

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Run on:

Sequence:

Searched:

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Sequence 2, Application US/10109886
Publication No. US20020119499A1
GENERAL INFORMATION:
APPLICANT: TANABE SETYAKU CO. LTD.
APPLICANT: TANABE SETYAKU CO. LTD.
TITLE OF INVENTION: METHOD FOR IDENTIFYING OR SCREENING AGONIST AND TITLE OF INVENTION: ANDAGONIST TO PPAR
FILE REPERENCE: TANIGUCHI=6
CURRENT APPLICATION NUMBER: US/10/109,886
CURRENT APPLICATION NUMBER: 09/514,247
PRIOR APPLICATION NUMBER: PCT/JP98/03734
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1997-08-24
PRIOR FILING DATE: 1997-08-24
PRIOR FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Version 3.0
SEQ ID NO 2
SEG ID NO 2
SEG ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Artificially synthesized primer sequence US-10-109-886-2
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Similarity 75.8%; Pred. No. 2e+04;
25; Conservative 0; Mismatches 8;
                                      US-10-447-839A-78
US-09-989-722-251
US-09-989-722-251
US-09-989-727-251
US-09-989-737-251
US-09-989-737-251
US-09-990-442-251
US-09-991-16-251
US-09-991-16-251
US-09-991-16-251
US-09-991-16-251
US-09-991-251
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US-09-997-666-251
US-09-990-438-251
US-09-990-562-251
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US-09-997-653-251
US-09-993-667-251
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ORGANISM: Artificial Sequence
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Sequence 19, Appl
Sequence 19, Appl
Sequence 2676, Ap
Sequence 1287, Ap
Sequence 1287, Ap
Sequence 23, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 15, Appl
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                                                                                                                           February 29, 2004, 11:52:38; Search time 267.801 Seconds (without alignments) 9052.319 Million cell updates/sec
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672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_MBW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NBW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NBW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/US08_NBW_PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NBW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10N_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10N_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10N_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-933-346-463

SUS-10-131-827-677

US-10-119-31-8

SUS-10-131-827-309

US-09-817-464-19

US-10-331-289-19

US-10-331-289-19

US-10-131-827-1362

US-10-131-827-1362

US-09-978-917A-23

US-09-978-917A-23

US-09-978-917A-23

US-09-978-917A-23

US-09-978-917A-23

US-09-978-917A-23

US-10-138-195-31
                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                            2353733 seqs, 1803733377 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                           using sw model
                                                                                                                                                                                                                                                                                   IDENTITY_NUC Gapopt 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0 Maximum DB seq length: 50
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Match
                                                                                                                                                                                                                          Perfect score:
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Database :

Result 0

Sequence 251, 1 Sequence 251, 1 Sequence 251, 1 Sequence 251, 1

sequence Seq

Sequence Sequence

Sequence

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Gaps

ö 35;

Length Indels

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APPLICANT: WITE, ALISON
APPLICANT: WARWIN, BRIAN C.
APPLICANT: VARWING
APPLICANT: OLAN, ZUEMING
APPLICANT: OLAN, ZUEMING
TITLE OF INVENTION: ANTIBODIES AND OTHER SELECTIVE IL-1 BINDING AGENTS THAT ALLOW BI:
TITLE OF INVENTION: IL-1 RECEPTOR BUT NOT ACTIVATION THEREOF
FILE REFERENCE: A-731
CURRENT APPLICATION NUMBER: US/10/011,931
                                                                                         APPLICANT: Fry, Kirk
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc's
APPLICANT: Ly, Ngoc's
FILE PEPERBORNIC INFLAMMATORY DISBASES
FILE REPERBORNICS: 506612000120
CURRENT APPLICATION NUMBER: US/10/131,827
CURRENT FILING DATE: 2002-09-06
PRIOR FILING DATE: 2001-10-22
PRIOR FILING DATE: 2001-16-08
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9090
SOFTWARE: Patentin version 3.1
SEQ ID NO 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Sequence 56, Application US/10319315

Publication No. US20030219774A1

GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
ITITLE OF INVENTION: NOVEL HUMAN NEUROTRANSMITTER TRANSPORTER
FILE REFERENCE: DO205 NP
CURRENT APPLICATION NUMBER: US/10/319,315

CURRENT FILING DATE: 2002-12-13

NUMBER OF SEQ ID NOS: 135

SOFTWARE: Patentin version 3.1

SEQ ID NO 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 3.0%; Score 20; DB 15; Length 50; 1 Similarity 82.1%; Pred. No. 2.6e+04; 23; Conservative 0; Mismatches 5; Indels
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Pred. No. 2.8e+04;
0; Mismatches 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 gccgggargggaaagacagaagaag 43
Sequence 677, Application US/10131827
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.9%;
Best Local Similarity 69.2%;
Matches 27; Conservative
                          US20040009479A1
                                                                          APPLICANT: Wohlgemuth, Jay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-319-315-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 23; Conserv
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US-10-011-931-8/c
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0
                                          Sequence 463, Application US/09993346
Publication No. US20030124530A1
GENERAL INFORMATION: Edwards, Cynthia A.
Cantor, Charles R.
Andrews, Beth M.
Turin, Lisa M.
Fry, Kirk E.
TILLE OF INVENTION: Sequence-Directed DNA Binding
Molecules, Compositions and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MCBLUM IIEE FLODY GUENE
COMPUTER: IEM PC Compatible
COMPUTER: IEM PC COMPACIBLE
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/993.346
FILING DATE: 13-No. US20030124530A1-2001
PRIOR APPLICATION NUMBER: 09/354,947
FILING DATE: CURNOWN:
APPLICATION NUMBER: US 08/171,389
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: US 07/996,783
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: US 07/996,783
FILING DATE: 27-UN-1991
APPLICATION NUMBER: US 07/996,783
FILING DATE: 27-UN-1991
APPLICATION NUMBER: US 07/996,783
FILING DATE: 27-UN-1991
ATTORNEY/AGENT INFORMATION:
NUMBER: US 08/081,070
FILING DATE: 22-UN-1993
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 39,118
REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1
TELECOWNUNICATION INFORMATION:
TELEPHONE: (650) 324-0880
TELEFAX: (650) 324-0960
                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CIIY: Redwood City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
;
US-09-993-346-463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 50 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 463: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                  NUMBER OF SECUENCES: 664
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Best Local Similarity 65.9
Matches 29; Conservative
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                          -09-993-346-463/c
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RESULT 3 US-10-131-827-677

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APPLICANT: Kuhn, Ranier
APPLICANT: Lindaur, Kristen
APPLICANT: Wonpfel, Thomas
TITLE ON INVENTION: HUMAN Metabotropic Glutamate Receptor Subtypes (HMR4,
TITLE OF INVENTION: HMR6, HMR7) and Related DNA Compounds
TITLE OF INVENTION: HMR6, HMR7) and Related DNA Compounds
TITLE REPRENCE: 4-19679/A/PCT
CURRENT APPLICATION NUMBER: US/10/331,289
CURRENT APPLICATION NUMBER: PCT/EP94/02991
PRIOR APPLICATION NUMBER: PCT/EP94/02991
PRIOR APPLICATION NUMBER: EPO 9416553.7
PRIOR APPLICATION NUMBER: EPO 9416553.7
PRIOR FILING DATE: 1994-09-07
PRIOR FILING DATE: 1993-09-20
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 19
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                                                                                                                                                                                                                                                                                                                                                                                                                           Score 19.2; DB 9; Length 44;
Pred. No. 4.5e+04;
0; Mismatches 13; Indels
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) OTHER INFORMATION: Oligonucleotide primer

US-10-331-289-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  266 CACACCCTGCTCCAGCAGGCTCTCCGGCTGCCCCTGC 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42 cccocrccracccraccadecccracceccccccccade 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266 CACACCCTGCTCCAGCAGGCTCCCGGCTGCCCCTGC
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          ; EARLIER FILING DATE: 1996-03-19
; EARLIER APPLICATION NUMBER: EPO 9416553.7
; EARLIER FILING DATE: 1994-08-19
; EARLIER PELING NUMBER: EPO 93810663.0
; EARLIER FILING DATE: 1993-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PALENTIN VET. 2.0
; SOFTWARE: PALENTIN VET. 4.0
                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 2676, Application US/10349143; Publication No. US20040005584A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19, Application US/10331289
Publication No. US20030113868A1
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 67.5%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Flor, Peter J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: FFY, KIK
APPLICANT: Woodward, Robert
TITLE OF INVENTION: GRRONIC INFLAMMATORY DISEASES
TITLE OF INVENTION: GRRONIC INFLAMMATORY DISEASES
UNRENT APPLICATION NUMBER: US/10/131,827
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9090
NUMBER OF SEQ ID NOS: 9090
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APPLICANT: Flor, Peter J.
APPLICANT: Kuhn, Ranier
APPLICANT: Lindaur, Kristen
APPLICANT: Lindaur, Kristen
APPLICANT: Puttner, Irene
APPLICANT: Puttner, Irene
APPLICANT: Wopfel, Thomas
TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4, ITTLE OF INVENTION: HMR6, HMR7) and Related DNA Compounds
FILE REFERENCE: 4-19679/A/PCT
CURRENT PELICALION NUMBER: US/09/817,464
CURRENT FILING DATE: 2001-03-26
EARLIER APPLICATION NUMBER: US/09/617,785
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 2.9%; Score 19.4; DB 15; Length 1 Similarity 64.4%; Pred. No. 4e+04; 29; Conservative 0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45 AGAAGAAGCGGGGATACTTGGTTCAAGCCCTGACACGAAGAATA 1
                                                                                                                                                                                                                                                                                                                                        Score 19.6; DB 14;
Pred. No. 3.5e+04;
0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                           331 GAAGAGCTCCAGGAACTTGGCATTCCTCAGGATC 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAACACCAGCAGGAACCAGGTGTTCCTCAAGATC 17
CURRENT FILING DATE: 2002-04-01
PRIOR PEPLICATION NUMBER: US 60/244,118
PRIOR FILING DATE: 2000-10-27
NUMBER OF SEQ 1D NOS: 78
SEQ ID NO 8
LENGTH: 50
                                                                                                                                                                                                                                                            OTHER INFORMATION: KAPPA CHAIN CHIMERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/10131827
o. US20040009479A1
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; Patent No. US20020127638A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) ORGANISM: Arabidopsis thaliana US-10-131-827-309
                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 73.5%;
Matches 25; Conservative (
                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wohlgemuth, Jay APPLICANT: Fry, Kirk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 309, Application No. US200 GENERAL INFORMATION:
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APPLICANT: FTY, Kirk
APPLICANT: FTY, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Ly Ngoor Conserved the North Report Conserved the North Report Conserved the North Report Conserved the North Contended the North Conserved the North Conserved the North Conserv
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US-09-978-917A-23
i Sequence 23, Application US/09978917A
j Sequence 23, Application US/09978917A
j Publication No. US20030027299A1
j GENERAL INFORMATION:
j GENERAL INFORMATION:
j TITLE OF INVENTION: Protein C or activated protein C-like molecules
j TITLE OF INVENTION: Protein C or activated protein C-like molecules
j CURRENT PAPLICATION NUMBER: US/09/978,917A
j CURRENT FILING DATE: 2001-10-17
j NUMBER OF SEQ ID NOS: 48
j SOFTWARE: Patentin Ver. 2.1
j SEQ ID NO 23
j LENGTH: 50
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Publication No. US20030207340A1
GENERAL INFORMATION:
APPLICANT: Morre, Dorothy J.
APPLICANT: Chueb, Pin-ju
TITLE OF INVENTION: Sequences Encoding Human Neoplastic Marker
FILE REFERENCE: 85-99
CURRENT APPLICATION NUMBER: US/10/138,195
CURRENT FILING DATE: 2002-05-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-978-917A-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           465 CCGGTGGCGGGTGGACGTGGCCATCTCAACCAGCGCTCAGTCCCGC 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 coccidecaderocrecrearcaactaacaaaaactagccrec 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178 CATGGGAAAGACTGCAGAGAAGCTGTGGAGCAACTTGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 19.2; DB 15;
Pred. No. 4.7e+04;
0; Mismatches 13;
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Publication No. US20040009479A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 63.0%
Matches 29, Conservative
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Dest Local Similarity 67.5%
Matchès 27, Conservative
                                                                 APPLICANT: Wohlgemuth, Jay
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CORGANISM: Homo sapiens
US-10-131-827-1362
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APPLICANT: Woodward, Robert
APPLICANT: Ly, Nago:
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
FILE REPERENCE: 5066212000120
CURRENT APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-06-08
PRIOR FILING DATE: 2001-06-08
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9090
SOFTWARE: Patentin version 3.1
LENGTH: 50
                                      APPLICANT: Chumakov, 11ya

JAPLICANT: Chumakov, 11ya

TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERRANCE: GENSET. 020CP1

CURRENT APPLICATION NUMBER: US/10/349,143

CURRENT FILING DATE: 2003-01-21

PRIOR PILING DATE: 1999-10-20

PRIOR PLILING DATE: EARLIER APPLICATION NUMBER: US 60/298,850

PRIOR PILING DATE: EARLIER FILING DATE: 1999-04-21

PRIOR PILING DATE: EARLIER FILING DATE: 1998-04-21

PRIOR PILING DATE: EARLIER FILING DATE: 1998-04-21

PRIOR PILING DATE: EARLIER FILING DATE: 1998-04-21

NUMBER OF SEQ ID NOS: 11796

LENGTH: 47
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Publication No. US20040009479A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 27; Conserv
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LOCATION: 24
OTHER INFORMATION:
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US-10-131-827-1287
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Sequence 1362, Application US/10131827

RESULT 11 US-10-131-827-1362/c

Gaps

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2.8%; Score 18.6; DB 14; Length 43; 65.9%; Pred. No. 6.9e+04; ive 0; Mismatches 14; Indels
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Job time : 270.801 secs
                      CURRENT APPLICATION NUMBER: US/10/176,255
                                  FRIOR PELLING DATE: 2002-06-19
FRIOR PELLING DATE: 1998-04-14
FRIOR PILING DATE: 1998-04-14
FRIOR APPLICATION NUMBER: 09/76/,013
FRIOR APPLICATION NUMBER: 09/76/,013
FRIOR APPLICATION NUMBER: 09/292,072
FRIOR APPLICATION NUMBER: 09/292,072
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.1
SEQ ID NO 15
LENGTH: 43
                                                                                                                                                                                                                                                                                               TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

COTHER INFORMATION: synthetic construct

US-10-176-255-15
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Best Local Similarity 65.9
Matches 27; Conservative
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APPLICANT: Liaw, Chen W.
APPLICANT: Russo, Joseph F.
TAPLICANT: Thomsen, William F.
TITLE OF INVENTION: No. US20030153004A1-Endogenous, Constitutively Activated Human Se
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US-10-138-195-31
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APPLICANT: Morre, D. James
APPLICANT: Morre, D. James
APPLICANT: Chuch, Pin-ju
TITLE OF INVENTION: Sequences Encoding Human Neoplastic Marker
FILE REFERENCE: 85-99
CURRENT PAPLICATION NUMBER: US/01/0130,195
CURRENT FILING DATE: 2002-05-01
PRIOR FILING DATE: 1999-11-01
PRIOR PLING DATE: 1999-11-01
PRIOR FILING DATE: 2000-01-01
SPIOR APPLICATION NUMBER: 2000/30190
PRIOR FILING DATE: 2000-11-01
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 32
LENGTH: 38
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                                                                                                                                                                                                                                                                                                                                                                    Length 38;
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2.8%; Score 18.6; DB 15;
Best Local Similarity 72.7%; Pred. No. 6.7e+04;
Matches 24; Conservative 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         358 CAGGATCTAATTGGAGATTTGGCCAGTTTGGCA 390
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PRIOR APPLICATION NUMBER: 1999-11-01
PRIOR APPLICATION NUMBER: PCT US00/30190
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 31
LENGTH: 38
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Publication No. US20030207340A1
GENERAL INFORMATION:
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No. US20030153004A1
                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                      1 Similarity 72.7 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : AREN-0328
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Publication No.
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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	nucielo searon, using sw model		
Run on: Fe	ebruary 29, 2004, 10:05:33 ; Search t (without al 10688.739 M	h time 2724.97 Seconds alignments) 9 Million cell updates/sec	
Title: US Perfect score: 67 Sequence: 1	US-09-904-568-1_COPY_132_803 672 1 atgtctgctttgggggctgcgtgagc	.grgagcgaaactgcaggac 672	
Scoring table: ID	IDENTITY NUC Gapop 10.0 , Gapext 1.0		
Searched: 34	3470272 seqs, 21671516995 residues		
Total number of hi	hits satisfying chosen parameters:	1603530	
Minimum DB seg len Maximum DB seg len	.ength: 0 .ength: 50		
Post-processing: M M	Minimum Match 0% Maximum Match 100% Listing first 45 summaries		
Database	GenEmbl:* : gb_ba:* : gb_ba:* : gb_bre:* : gb_ov:* : gb_ov:* : gb_br:* : gb		

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

D)	Result No. S	core	Query Match	Length	DB	QI	Desc	cription
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		21.4	•	20	9	BD174394	BD1.	74394 Cell use
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		ο,		46	φ	AR157914	ARI	57914 Sequence
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t)		6	•	32	9	BD061703	BDO	51703 Antigeni
		2.0	•	4 4	oυ	AR149584	ARI	19584 Sequence
		; ⊣		27	9	AR089960	ARO	39960 Sequence
υ	24	19	٠	27	9	AR196995	AR1	6995 Sequence
		Н,	•	27	9	AR259149	AR2	9149 Sequence
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		ο α	•	1 4 0 C	0 -	AA466471	77.0	10471 3644611C
		18.8		n N	9 19	BD225137	BD22	BD225137 Polymorph
		œ.		43	9	AR107092	AR1	7092 Sequence
		<u>.</u> ه	٠	43	y v	AR111855	ARI	1855 Sequence
		σα	٠	4.4	ט מ	AK1183/2 AK1183/2	ARI	183/2 Sequence
				4.4	ω	AX813374	AX8	3374 Sequence
		œ.		43	9	BD132482	BD13	12482 Binding
		٠ د		47	ω ·	AX236856	AX2	16856 Sequence
				3. L	ע מ	AX286510	AAZ	3336 Seguence
		. a		3 7	o vo	AR012348	ARO	2348 Sequence
				37	w	BD069047	BDOG	9047 Hematopo
		8		39	9	E49257	E492	257 Omega 3 fat
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Ü				47	o u	3 3	1771	2 Sequence
	4 4 4 10	18.4	2.7	4 S 0 O	φα	AX582839 AR252548	AX582 AR252	82839 Sequence 52548 Sequence
						ALIGNMENTS		
(3) 44	RESULT 1 AX404880/c							
υu	LOCUS		7	3 from	Patent	49 bp ent WO0222833.	DNA linear	PAT 14-JUN-2002
Uβ	ACCESSION		AX404880			0		
3 54	KEYWORDS				ב ב	2		
5 C	SOURCE	synt	synthetic c	construct	1 to			
		art	ficial	segmence	0			
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linear PAT 14-JUN-200					Pfizenmaier, K., Wuest, T., Moosmayer, D., Grell, M. and Scheurich, P.	Fusion protein from antibody cytokine-cytokine inhibitor (selectokine) for use as target-specific prodrug	
DNA					, ם,	ine-c	
49 bp	WO0222833.				, Моовшауел	usion protein from antibody cytokine-cytokine i selectokine) for use as target-specific prodrug	Patent: WO 0222833-A 13 21-MAR-2002;
	Sequence 13 from Patent W00222833. AX404880	struct	struct quences.		., Wuest, T.	n from anti for use as	22833-A 13
	13 F	o con	c cons		ier, K	roteir kine)	NO 023
AX404880	Sequence AX404880	synthetic construct	synthetic construct artificial sequences	1	Pfizenma	Fusion p: (selecto	Patent: 1
RESULT 1 AX404880/c LOCUS	DEFINITION ACCESSION	KEYWORDS	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL

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E14011
E14011.1 GI:5708694
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Cell useful for evaluation of action of sex hormone receptor.
BD174394
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SALTIficial Sequence

BN JP 200247986-A/27

PN JP 200247986-A/27

PF 23-FEB-2001

PF 23-FEB-2001

PF 23-FEB-2001

PF 23-FEB-2001

CINCLOP, CINCLOP, CIQU/02, CIQU/66// (CIZNS/00, CIZNS/00, PC (CIZNS/00, CIZNS/19)), CIZQI/66// (CIZNS/00, CIZNS/19))

CC Description of Artificial Sequence:Primer

FH Key

Location/Qualificat

FT source

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                              1. .49
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/db_xref="taxon:32630"
/noce="Primer 4 fuer die Amplifikation eines humanen
TNF-Fragments"
                                                                                                                                                                                     Gaps
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synthetic construct
artificial sequences.

I (bases 1 to 50)
Nakao, T., Matsue, K. and Takebayashi, N.
Cell useful for evaluation of action of sex hormone receptor
Patent: JP 2002247986-A 27 03-SEP-2002;
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Universitaet Stuttgart (DE) ; Pfizenmaier, Klaus (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 AGCTTCTGCGGCACGCTGTTGACGCTGTTAAGCGGGTCGCTGCAGGG 50
                                                                                                                                                   Match 3.2%; Score 21.8; DB 6; Length 49; Local Similarity 70.7%; Pred. No. 8.1e+05; es 29; Conservative 0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Length 50;
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                                                                                                                                                                                 12; Indels
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/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"
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Sequence 808 from patent US 6528260.
AR284756
AR284756.1 GI:29721660
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JP 2002247986-A/27.
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Unclassified.
1 (bases 1 to 47)
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AR284756/c
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BD174394
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Blumenfeld,M., Chumakov,I., Bougueleret,L. and Cohen,A.
Biallelic markers related to genes involved in drug metabolism
Patent: US 6528260-A 808 04-MAR-2003;
Location/Qualifiers
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/organism='Artificial sequences'.
Location/Qualifiers
                                                                                                                                                                                                 Length 47;
                                                                                                                                                                                                                                                                                       96 AGTGACGCCGTGGCTCAGCTCTTGAAGGACTTAGACAGGAGCA 139
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                                                                                                                                                                                              Query Match
3.2%; Score 21.2; DB 6; Length 4
Best Local Similarity 65.9%; Pred. No. 1.2e+06;
Matches 29; Conservative 1; Mismatches 14; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unidentified
unidentified
unclassified.
1 (bases 1 to 40)
Shimada,K. and Namatame,Y.
IMMOBLIZATION OF GRNE
Patent: JP 1997257798-A.1 03-OCT-1997;
SUMITOMO METAL IND LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Artificial sequences.
JP 1997257798-A/1
03-0CT-1997
19-MAR-1996 JP 1996062885
SHIMMADA YAZUNORI, NAMATAME YASUKO
GOIN33/566,CI2N15/09,CI2Q1/68;
strandedness: Single;
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Seguence 249 from Patent EP1288296.
AX710949
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/db_xref="taxon:32644"
                                                                                                             /organism="unknown"
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hypothetical: No;
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PAT 31-JAN-2002
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A61K39/145,A61K39/21,A61K39/23,A61K39/245,A61K39/29,A61K48/00,
A61P1/16,
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C12N15/09, C12N5/10, C12N7/00//A61K38/43, A61K39/125, A61K39/13,
                                                                                                                                                 Gaps
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07/882824 PR
07/882921 PR
07/882921 PR
07/884073 PR
07/884431 PR
07/884521 PR
07/984521 PR
07/9485431 PR
07/94854 PR
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1 (bases 1 to 42)

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14-MAY-1992 US 07/88283,14-MAY-1992 US 07/882814

14-MAY-1992 US 07/882886,14-MAY-1992 US 07/882818

14-MAY-1992 US 07/88289,14-MAY-1992 US 07/882818

14-MAY-1992 US 07/88292,14-MAY-1992 US 07/883823

14-MAY-1992 US 07/88292,14-MAY-1992 US 07/883823

14-MAY-1992 US 07/88494,14-MAY-1992 US 07/884313

14-MAY-1992 US 07/884426,14-MAY-1992 US 07/88431

14-MAY-1992 US 07/884436,14-MAY-1992 US 07/88431

14-MAY-1992 US 07/884436,14-MAY-1992 US 07/88431

15-OCT-1992 US 07/936086,18-SEP-1992 US 07/935884

15-OCT-1992 US 07/936086,18-SEP-1992 US 07/949359

15-OCT-1992 US 07/93738,07-DEC-1992 US 07/981359

07-DEC-1992 US 07/98732,07-DEC-1992 US 07/987129
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                                                                                Length 42;
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3.1%; Score 20.8; DB 6;
Best Local Similarity 70.0%; Pred. No. 1.5e+06;
Matches 28; Conservative 0; Mismatches 12;
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/organism="synthetic construct"
/mol_type="genomic RNA"
/db_xref="taxon:32630"
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01-MAY-2000 JP 2000132651
11-MAY-1992 US 07/8826
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synthetic construct
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Matches 28; Conserva
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PC C12N
PC A61K
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PC A61P
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ACCESSION
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JOURNAL
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BD001519
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07/882824 PR
07/882821 PR
07/883823 PR
07/88433 PR
07/88433 PR
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synthetic construct
synthetic construct
artificial sequences.

(bases 1 to 42)
Braper,K.G., Dadyktz,L.W., Macswigen,J.A., Maysejak,D.G.,
Holesek,J.G. and Mamone,A.J.
Method and reagent for inhibiting viral replication
Patent: JP 2000342285-A 250 12-DEC-2000;
Artificial Sequence
OS Artificial Sequence
Py 2000342285-A/250
                                                                                                  Draper, K.G., Mcswiggen, J.A., Holecek, J.J., Dudycz, L.W., Macejak, D.G. and Mamone, J.A.
Method and reagent for inhibiting HBV viral replication Hethot: EP 128296-A 249 05-MAR-2003;
RIBOZYME PHARMACEUTICALS, INC. (US)
Location/Qualifiers
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Location/Qualifiers
1. .42
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
3.1%; Score 20.8; DB 6; Length 42;
Best Local Similarity 70.0%; Pred. No. 1.5e+06;
Matches 28; Conservative 0; Mismatches 12; Indels '
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BD001090 42 bp RNA linear Method and reagent for inhibiting viral replication.
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                                                                                                                                                                                                                                                                                                              1. .42
/organism="Human herpesvirus 5"
/mol_type="unassigned RNA"
/db_Xref="taxon:10359"

    42
    ^2 organism="synthetic construct"
/mol type="genomic RNA"
/db_xref="taxon:32630"

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C12N5/00, (C12N5/00,C12R1:91)
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11-MAY-1992 US 07/8826
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JP 2000342285-A/250.
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15-OCT-1992 US
07-DEC-1992 US
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31-JUL-1992
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BD001090
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L JUNKO MINAKAMI, TOMOYASU TANIGUCHI
C C12N15/09, C12N1/19, C12Q1/68//(C12N1/19, C12R1:645), C12N15/00 CC
Strandedness: Single;
Topology: Linear;
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                                Unclassified.

1 (bases 1 to 47)

Blumenfeld,M., Chumakov,I., Bougueleret,L. and Cohen,A.

Biallelic markers related to genes involved in drug metabolism

Patent: US 6528260-A 639 04 MAR-2003;

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                      596 AGCTGCGGTACAGTGTAGCCTTGGTCCTTAAGGAGATGGCAGAAC 640
                                                                                                                                                                                                                                                                                                                                                           3 AGGTAGGGGACAGTGAAGCATKGGGGGGCCCAGGAGCTGCCAGAGC 47
                                                                                                                                                                                                                                           Query'Match 3.1%; Score 20.6; DB 6; Length 4 Best Local Similarity 64.4%; Pred. No. 1.7e+06; Matches 29; Conservative 1; Mismatches 15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Method for screening PPAR agonist and antagonist Patent: JP 1999056369-A 2 02-MAR-1999; TANABE SEIYAKU CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ce 1. .35
/organism='Unidentified'
Location/Qualifiers
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llarity 75.8%; Pred. No. 2.2e+06;
Conservative 0; Mismatches 8;
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Sequence 2 from patent US 6365361.
AR203329
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/organism="unidentified"
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/db_xref="taxon:32644"
                                                                                                                                                   1. .47
/organism="unknown"
/mol_type="genomic DNA"
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1 (bases 1 to 35)
Junko,M. and Tomoyasu,T.
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JP 1999056369-A/2
02-MAR-1999
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Best Local Similarity
Matches 25; Conserv
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AR203329
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Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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Patent: WO 02052044-A 484 04-JUL-2002;
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Patent: WO 02052044-A 6666 04-JUL-2002;
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Sequence 639 from patent US 6528260.
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Sequence 484 from Patent WO02052044.
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                      1 (bases 1 to 35)
Taniguchi T. and Mizukami, J.
Method for identifying or screening agonist and antagonist to PPAR
Patent: US 6366361-A 2 02-APR-2002;
Location/Qualifiers
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Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E.
Method of determining DNA sequence preference of a DNA-binding
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Location/Qualifiers
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129591.1 GI:1820382
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Edwards, C.A., Cantor, C.R., Andrews, B.M. and Turin, L.M.
Screening assay for the detection of DNA-binding molecules
Patent: US 5726014-A 463 10-MAR-1998;
Location/Qualifiers
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                                       259 GCGGGCACACACCCTGCTGCAGCAGGCTCTCCGGGCTGCCCCC 302
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65.9%; Pred. No. 2.4e+06;
tive 0; Mismatches 15;
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BM397151 5009-0-2
BM397161 6003072180
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AU106355 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone KAT02155, mRNA sequence.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 50)
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EMBO Rep. 2 (5), 388-393 (2001)
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1-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

1-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yeuzukianeu-nokoyo.ac.jp

Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and

Sugano,S. Construction and characterization of a full

length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),

149-156 (1997).
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Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

Location/Qualifiers
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1 (Dases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Tofa,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y. Suyama,A. and Sugano,S., Okubo,K., Diverse transcriptional initiation revealed by fine, large-scale EMBO Rep. 2 (5), 388-393 (2001)
                                                                                                                                                                                                                                                            Gaps
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/mol_type="mRNA"

/db_txref="txxxon:9606"

/clone="HRC05721"

/clone="HRC05721"
                                                                          1. .50
/organism="Homo sapiens"
/organism="mRNA"
/db xref="taxon:9606"
/clone="XATOSI55"
/clone=lib="Sugano Homo sapiens cDNA library"
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                                                                                                                                                                                                                       3.3%; Score 22; DB 9; Length 50;
llarity 73.7%; Pred. No. 3e+05;
Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                 264 CACACACACCTGCTCCAGCAGGCTCTCCGGCTGCCCC 301
                                                                                                                                                                                                                                                                                                                                   270 CACCCTGCTCCAGCAGGCTCTCCGGCTGCCCCTG 304
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Homo sapiens
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Best Local Similarity 74.3
Matches 26; Conservative
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Matches 28; Conserv
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AA933650/c
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AUTHORS
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Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.

Bmail: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Bmmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue type="pooled germ cell tumors"

/lab host="DH108"
/clone_lib="NGI_CGAP_GC4"
/note="Vector: pT713D-Pac (Pharmacia) with a modified
polylinker, 1st strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
germ cell tumors, and was then primed with a Not I -
oligo (4T) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo. "
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similar to SW:DPD2_HUMAN P49005 DNA POLYMERASE DELTA SMALL SUBUNIT; , mRNA sequence.
AA933650
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Railam, H., Longacre, S., Mahmoud, M., Menen, E., Pedersen, T., Reilly, M., Rosack, K., Stokes, R., Stokes, R., Stokes, R., Von Niederhausern, A. and Wright, D., Weiss, R.
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2M0244N12R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0244N12 R, genomic survey sequence.
AZ971265
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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/clone="IMAGE:1551178"
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Mus musculus
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GSS.
                                                                                                                     AA933650.1 GI:3089918
                                                                                                                                                                                       Homo sapiens (human)
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50 bp mRNA linear EST 30-AUG-2001
AU104331 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
COLF0073, mRNA sequence.
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
5-6-1, Shirokane, --Cohyo, ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
1-ength-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
                                                                                                                      Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yauzuki@ins.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
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Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
piperse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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/dlone="colo0994"
/clone_lib="Sugano Homo sapiens cDNA library"
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3.0%; Score 20.4; DB 9; Length 50;
Best Local Similarity 71.1%; Pred. No. 7.4e+05;
Matches 27; Conservative 0; Mismatches 11; Indels
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/organism="Homo sapiens"
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Mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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/db_xref="taxon:9606"
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Location/Qualifiers
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Best Local Similarity 77.4%; Pre
Matches 24; Conservative 0;
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                                                                                                             Contact: Yutaka Suzuki
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1 (Sese 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Bata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
                                                                                                                                                      Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lab_host="B. coli strain XL10-Gold, T1-resistant, F-"
Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                     Plate: 0244 row: N column: 12
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Mus musculus"
                                           Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mol_type="genomic DNA"
|strain="C57BL/6J"
|db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone="UUGC2M0244N12"
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Homo sapiens
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AU106354/c
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Gaps

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Gaps

RESULT 7 AL757838/c LOCUS DEFINITION

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KEYWORDS SOURCE ORGANISM

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REFERENCE

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FEATURES

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/tissue type="hypothalamus"
/tissue type="hypothalamus"
/tissue type="hypothalamus"
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/tissue type="hypothalamus"
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/clone lib="MilH MGC 96"
/clone lib="MilH MGC 96"
/clone lib="MilH MGC 96"
/clone lib="MilH MGC 19"
/clone li
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National Institutes of Health, Mammalian Gene Collection (MGC)

Introductional Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Miklos I.M.A.G.E. Consortium (LIML)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Library

Hup://image.llnl.gov m. column: 23
41 bp mRNA linear EST 12-SEP-2001
mRNA sequence.
BI669410
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603242001Fl NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5284488 5',
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1 (Joses 1 to 47)
NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                           Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bummalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 41)
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Location/Qualifiers
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/db_xref="taxon:9606"
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BIS44737.1 GI:15432049
                                                                                                                                                                                     BI669410.1 GI:15583643
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/mod_type="genomic DDA"
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/clone="Ib="Arabidopsis thaliana T-DNA insertion lines"
/clone llb="Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAcle1. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thalaina nuclear genome sequence were processed for submission. T-DNA derived sequences were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                             AL757838 18-JUN-2002 Arabidopsis thaliana T-DNA flanking sequence GK-152H09-013139, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryofa, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B. A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strizhov,N., Li.Y., Rosso,M. and Weisshaar,B.

Direct Submission

Direct Submission

Direct Submission

Submitted (17-707-2002) Weisshaar B., Max-Planck-Institut fuer

Zubchitungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

This sequence is recovered from the left border of the T-DNA. It

indicates an insertion close to or within gene At4g18700. The

sequences are generated at the MPI for Plant Breeding Research in

the context of the GABI-Kat project. GABI-Kat is part of the Germa

Plant Genomics program designated 'GABI'. Information on line

availability can be found at:

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and Weisshaar, B.
A pipeline for automated high-throughput generation of FSTs
(flanking sequence tags) from Arabidopsis thaliana T-DNA
transformed lines
Unpublished
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Pred. No. 1.1e+06;
0; Mismatches 9;
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/mol_type="genomic DNA"
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                                                                                       629 AGATGGCAGAACTGGAGAAGAAGTGTGAGCG 659
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Arabidopsis thaliana
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RESULT 8 BI669410/c

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ORIGIN

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organism="Homo sapiens"
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Best Local Similarity 70.3
Matches 26; Conservative
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/clone lib="NIH MGC 95"
/clone lib="NIH MGC 95"
/note="Organ: brain_ Vector: pBluescriptR (modified pBluescript K8+); Site: 18 maHl; Site=2: SalI-XhoI (gtcgag); Oligo-dT primed using primer
5.-TTTTTTTTTTTTTTTVV-3, size-selected for average insert size 2: Skb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AU106356 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone KAT03974, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yeuzukidims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997):
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Inoyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
http://image.llnl.gov
High quality sequence stop: 47.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Primates; Catarrini; Hominidae; Homo.

1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites

EMBO.Rep. 2 (5), 388-393 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Pred. No. 1.3e+06;
                                                                                                                                                                                                                                                                                                                                                    /tissue_type="hippocampus"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             283 CAGGCTCTCCGGCTGCCCCTGCTAGTCT 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5284488"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.9%;
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Best Local S
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AU106356/c
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SOURCE
ORGANISM
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AUTHORS
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MEDLINE
PUBMED
COMMENT
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source

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/note="Vector: PRITE: Site 1: BamHI; Site 2: BamHI; Shotgun cloning of RDA difference products. Macrophage and foomcell libraries were submitted to successive rounds of subtractive hybridisations generating populations of gene fragments that are differentially expressed in macrophage to foam cell formation."
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                                                                                                                                                                                                                                                                                 EST 14-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identification of candidate genes in atherosclerosis - Virtual chi
analysis in RDA based transcript profiling of monocyte/macrophage
response to exidised LDL
Unpublished (2001)
Contact: Andersson Tove
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                              ьсэ14884
ОР2.0.138 Human THP1 cell line library Homo sapiens cDNA, mRNA
sequence.
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                                                     Gaps
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     50;
                                                  11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.9%; Score 19.4; DB 9; Length 70.3%; Pred. No. 1.3e+06; tive 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Teknikringen 34, plan 6, 100 44 Stockholm, Sweden Tel: 446 8 790 71 29 Fax: 446 8 24452 Email: tove@biochem.kth.se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170 GGGCCCTGCATGGGAAAGACTGCAGAGAAGCTGTGGAG 207
                                                                                                   258 GGCGGCACACACCCTGCTCCAGCAGGCTCTCCGG 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Department of Biotechnology
                                                                                                                                                                                                                                                                                                                                                                               BG314884.1 GI:18997731
                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
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26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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DEFINITION
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/organism=Drosophila melanogaster"
/organism=Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="teaxon:7227"
/done_lib="Drosophila melanogaster P lethal line"
/done_lib="Drosophila melanogaster prosophila
/note="Inverse PCF was performed on Drosophila
melanogaster strains each of which contains a single P
transposable element insertion that is thought to cause
either lethality or sterility. The resultant fragment for
each strain was directly sequenced to determine the
genomic sequence at the site of insertion. Details of the
protocols used can be found at
http://fruitfly.berkeley.edu/p_disrupt/inverse_pcr.html."
                        The P element insertion position is base 035 in the 42 bases. This insertion position refers to the first base of the 8 base target recognition sequence. Class: transposon-tagged. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 50)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Malmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A.; von Misderhausern, A. and Wright, D., Weiss, R.
Moiderhausern, A. and Wright, D., Weiss, R.
Moude whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ479659
1M0300B03R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0300B03 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
'clone_lib="Mouse 10kb plasmid UUGCIM library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.8%; Score 19; DB 28; L
Best Local Similarity 69.4%; Pred. No. 1.5e+06;
Matches 25; Conservative 0; Mismatches 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36 AGTACTATAATGGCTCCATNCCGCATACCGCCACAG 1
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Insert Length: 10000 Std Error: 0.00
Plate: 0300 row: B column: 03
Seg primer: CACACAGGAAACAGCTATGACC
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/strain="C57BL/6J"
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High quality sequence stop: 50.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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AZ479659/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION,
KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                              Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.ut-cokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
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                                                                                                                         Eukāryotā; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammālia; Butheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Bata,H., Tcaira,H., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S., Okubo,K., Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1(2)k08708 Drosophila melanogaster P lethal line Drosophila melanogaster genomic Sequence recovered from 5' end of P element, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota, Metazoa, Arthopoda, Hexapoda, Insecta, Pterygota,
Bukaryota, Metazoa, Arthopoda, Hexapoda, Insecta, Pterygota,
Bukaryota, Badopterygota, Diptera, Brachycera, Muscomorpha,
Bphydroidea, Drosophilae, Drosophila.
1 (Bases I to 42)
Spradling, A.C., Stern, D., Beaton, A., Rehm, E.J., Laverty, T.,
Mozdan, N., Misra, S. and Rubin, G.M.
The BDGP gene disruption project: Single P element insertions
Mutating 30% of Drosophila autosomal genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Pred. No. 1.5e+06;
0; Mismatches 13; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244 CTGGCCGTCCTGCTGGCGGGCACACACACCCTGCTCCAGC 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Berkeley Drosophila Genome Project
University of California, Berkeley
Las Building, Berkeley, CA 94720-3200, USA
Fax: 5106439947
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Sequence recovery method was inverse PCR.
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                          AU104702.1 GI:13554223
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AQ025866.1 GI:3266218
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Best Local Similarity 67.5%;
Matches 27; Conservative
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                                                                           Homo sapiens (human)
Homo sapiens
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(http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pWAP42 (gil 4712114 [gb]AP129072.1), a copy.number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
                                               musculus C57BL/6J (male) was obtained
Laboratory Mouse DNA Resource
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Gaps . Query Match
2.8%; Score 19; DB 28; Length 50;
Best Local Similarity 65.1%; Pred. No. 1.7e+06;
Matches 28; Conservative 0; Mismatches 15; Indels 548 CAGATGGATCTGCACACCCCTTCGAGGTGCCCATAGCCAAATT 590 49 CAGTTGGTTCTTCACAGCAATTCAACACTTTCCTTTACCAAATT 7 à 음

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AU106353 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone AU106353 AU106353.1 GI:13555874 COL00742, mRNA sequence Homo sapiens (human) Homo sapiens LOCUS ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 15 AU106353/c

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE AUTHORS

1 (bases 1 to 50)
Suzuki, Y., Tatra, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hara, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001) TITLE

1375929 JOURNAL MEDLINE PUBMED COMMENT

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Suzuki,Y., Yoshiromo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),

FEATURES

iocation/Qualifiers

.49-156 (1997)

ORIGIN

1..50 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="COL00742" /clone_lib="Sugano Homo sapiens cDNA library"

; 0 2.8%; Score 18.8; DB 9; Length 50; 68.4%; Pred. No. 1.9e+06; tive 0; Mismatches 12; Indels Conservative Query Match Best Local Similarity Matches 26; Conserva

Gaps

264 CACACACACCCTGCTCCAGCAGGCTCTCCGGCTGCCCC 301 49 cccaccacaaaccaacrcccccccrcccccccc 12 ઠે ద

Search completed: February 29, 2004, 14:40:12 Job time : 2036.49 secs